

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: October 4, 2001, 05:45:40 ; Search time 1846.2 Seconds
(without alignments)
12641.694 Million cell updates/sec

Title: US-09-445-614-1

Sequence: 2469
1 cacgagcgccgacgcgacct.....gctgctctggggtcccaat 2469

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 10228115 seqs, 4726426750 residues

Total number of hits satisfying chosen parameters: 20456230

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Oy	2020	atcgccctcatagcaggacgcgtcaaacagtctgcccaccagcaaacgtcggagctctggaa	2079
Db	1806	attgcccttatangtagactcttcAACACAGCTGGCCACTGACAAGCTGGAGCATCTGGAA	1865
Oy	2080	ctgcagaaaagccatctctgtcccttggaagatcgagaatgagtaagctatgtgtgtgcagaa-	2138
Db	1866	TTCGAGAAAAGCATTCTCTGTCTTTGGAGATGGAGANTGTTACTGGTGGTGCAAGAGAA	1925
Oy	2139	--gcagcggagcaggtgtgtactgtcacacgcttggcactaaagccagatggacgccgatgag	2196
Db	1926	AGGCATTCGGCGAGGAGAGCGCTCTGAAGATTGGCACCAAAGGGGATGGTATACCTGATGAG	1985
Oy	2197	cgcgtgtgcttaagaggtttggaagaggttgaaactgagcttaatggagcagaagctgtcctag	2256
Db	1966	CCTGTGTGCTTAAGAGGTGGAGGAAGTAACATGTGGCTGCTGATGGAGAGAAGACCTTCCAC	2045
Oy	2257	ctgtgttgaggaacccgtcacaggaggtgtccctcgaactcctcgaaacctgtctcgtcct	2316
Db	2046	TATATCTGAGGATCCATCAGGGGACAGGCATCACTGGTTTAAAAAAGACC-----	2094
Oy	2317	tccctcccaagagagatgataagatgtgtcctcttgagaaactatgtgtccccgtccagctc	2376
Db	2095	-CAACCTCTMAACCTGGGAGAAACAGTCCCTCAGAGAAACACATCTGCTTAGGTC	2153
Oy	2377	ctccgctccaactgtgtgtgcccagaatgcagcagcagga----ggccagagagcagaagcagaga	2432
Db	2154	CTCCAGCTCCCATCTGAGGCTCCACAGATGGCGGACAGCAGAGCTGGCGGGGTAGAGTGCGAA	2213
Oy	2433	tccttcacaacacatctgtctgtctgtg 2459	
Db	2214	TTTTGCCAGCCACACCCAGGCTACTG 2240	
RESULT	2		
AUI41855			
LOCUS	AUI41855	793 bp	mRNA
DEFINITION	AUI41855 THYRO1 Homo sapiens cDNA clone THYR1001346 5', mRNA	EST	25-OCT-2000
ACCESSION	AUI41855		
VERSION	AUI41855		
KEYWORDS	AUI41855.1 GI:11003376		
SOURCE	EST.		
ORGANISM	human.		
	Homo sapiens		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
REFERENCE	1 (bases 1 to 793)		
AUTHORS	Oka,T., Nishikawa,T., Suzuki,Y., Ishii,S., Saito,K., Kawai,Y., Yamamoto,J., Wakamatsu,A., Nakamura,Y., Nagai,T., Sugano,S. and Isogai,T.		
TITLE	HRI human cDNA project		
JOURNAL	Unpublished (2000)		
COMMENT	Contact: Takao Isogai Genomics Laboratory Helix Research Institute 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan Tel.: 81-438-52-3951 Fax: 81-438-52-3952 Email: genomics@hri.co.jp HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix Research Institute; cDNA library construction: Department of Virology, Institute of Medical Science, University of Tokyo, and Helix Research Institute. Location/Qualifiers: I. 793 /organism="Homo sapiens" /db_xref="taxon:9606" /clone="THYR1001346" /clone_1lb="THYRO1" /issue_type="thyroid gland" /note="Vector: pME18SF3"		
FEATURES			
Source			
BASE COUNT	184 a	229 c	230 g
ORIGIN		147 t	3 others

Query Match	27.9%	Score 668.6	DB 08	Length 793
Best Local Similarity	98.1%	Pred. No. 1.3e-155		
Matches 716	Conservative	0	Mismatches 12	Indels 2
Gaps				
QY	3	cgagcgccgacgcgcagctctggaggaagaagacccttgcacatctccatctgcacagag	62	
Db	65	CAACACCGACCGCGACGCTGGGAGGAAGAACCCCTTACATCTCCATCTCACAGAG	124	
QY	63	tcttgccttgcacccgagcagcctctctctctcttgcagtgatgacccctccagcttcag	122	
Db	125	TCTTGCTTGAGACCGAGCAGCACCCTCTCTCTCTAGATGAGACCTCACCCCTCCAGCTCTCAGT	184	
QY	123	tttcaagtttggagacatctgatctggagggcccaaaaatgtctcttggagcggaagggaaa	182	
Db	185	TTTCAAGTTGGAGACATTATGATGAGAGCCCAAAAGATGGCTTGAGGGCGGAGAGGAAA	244	
QY	183	gcttgcatttggagacgaggtctgctccctccatctgagtcacagcttccagggcgagacggaa	242	
Db	245	GCTGGAATTTGGAGAGGGGCTCTCTCCATGAGTACAGTTCAGGGCGAGAGACCGGAA	304	
QY	243	atctgcacctcagataagaagtlcaacctcaactaccgaaagggaacaggttgcagtcagcc	302	
Db	305	ATTTCGCCCTCAGATTAAGTGTCAACCTCAACTACACGAAAGGAAACAGGTGCCAGTCAGCC	364	
QY	303	ggatccaaacggatttgcagagatccgctctctcaatgcgtctcccggtgtgtcccca	362	
Db	365	GGATCCAAACCGATTGTGACCGGATCGGCTCTTCAATCGGTCTCCGGGGGTGTCCTCCGA	424	
QY	363	ggatctgctgtgacttccagagttaccctgcagacaagaccagcaagtaacctcacccagctgga	422	
Db	425	GGATCTGCTGACTTCCAGAGTACTCTAGACAGACACGAAAGTACTCTCACCGACTCGGA	484	
QY	423	atacagagaaggtctccacaggttaagaagtgctctgataagagctgtgctgaaaccttaaga	482	
Db	485	ATACACAAGAGGCTCCACAAGTAAACGTCGCTGATGAAGCTGTGTAACCTTAAGA	544	
QY	483	cggaatcaatccctgcattcttgcacatcttgcacatctgcagatcgacagggaatctggcaatccca	542	
Db	545	CGGAATCAATGCTCTGCATTTGCTGCATCTGCATGCATGCACAGGAGCTGTGGCAATCTTCA	604	
QY	543	ggcccttgtaaatggccacgtgtcacagatgactatccagagaccagcgcgtctgcacat	602	
Db	605	GCCTCTGTGTAATGGCCACGTGCACAGATGACTATTACGAGGACCCACAGCGCTCTGCACAT	664	
QY	603	cgccattgagaagagggaatctgcacgtgtgtgaagcttctctgttggagaatvgggccaatgt	662	
Db	665	CGCCATTGAGAAGAGGAACTGTGCATGTGTAACTTCTGTGTGAGATGGGGCCAAATGT	724	
QY	663	gcatgcggcgagcctgcgcgcgctctcttccagaaggccaaaggagcttgcatttccgg	722	
Db	725	GCAATGCC - GGCGTCGGGCG - TTNTTTCAGAANGGACAGGACTTGCTTTTAATGG	782	
QY	723	tgaagctacc 732		
Db	783	GAAAGCTACCC 792		

FEATURES	source
306	tccaaaccgaatttgaccggaatgsgccttcacatgsgtctccgggggtgtccccaggga 365
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205	atgtcaatgcttgcatttctccactctgcgaatcgcagacaggaactctgcacactcacc 146
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606	catlgaagaagaagatctcgaatgtgtgaagctcctcgtgtgaagaatctggggccaatttga 665
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666	tgccgggagcctcgggcgcg 684
25	tgccgggagcctcgggcgcg 7
RESULT 5	
LOCUS	BF732920 682 bp mRNA EST 30-MAR-2001
DEFINITION	nae17D01.x1 NCI-CGAP OV18 Homo sapiens CDNA clone IMAGE:3435576 3'
VERSION	similar to TR:09Y670 09Y670 VANILLOID RECEPTOR-LIKE PROTEIN . . .
KEYWORDS	RNA sequence.
ACCESSION	BF732920
VERSION	BF732920.1 GI:12057995
KEYWORDS	EST.
SOURCE	human.
ORGANISM	Homo sapiens
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
ORGANISM	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE	1 (bases 1 to 682)
AUTHORS	NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE	National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
JOURNAL	Tumor Gene Index
COMMENT	Unpublished (1997)
COMMENT	Contact: Robert Strausberg, Ph.D.
COMMENT	Email: cgaabs-remail.nih.gov
COMMENT	Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
COMMENT	R. Emmert-Buck, M.D., Ph.D. CDNA Library Preparation: M. Bento
COMMENT	Soares, Ph.D. CDNA Library Arrayed by: Christa Prange, The
COMMENT	I.M.A.G.E. Consortium DNA Sequencing by: Washington University
COMMENT	Genome Sequencing Center
COMMENT	Clone distribution: NCI-CGAP clone distribution information can be
COMMENT	found through the I.M.A.G.E. Consortium/LNL, send email to:
COMMENT	linfo@image.lnl.gov
COMMENT	Seq primer: -400p from Glbco
COMMENT	High quality sequence stop: 412.
COMMENT	Location/Qualifiers
COMMENT	1..682

BASE COUNT	ORIGIN
142 a	208 c 181 g 130 t 1 others

Query Match	24.1%	Score 596.2	DB 168	Length 682
Best Local Similarity	94.0%	Pred. No. 2.6e-133		
Matches 641	Conservative 0	Mismatches 39	Indels 2	Gaps 2

QY	727	ctaccgccctcttcttggccgctcttgacccaagaagrgggatgtgtgaaactccctcttgag	786
Db	2	CTAAGGCCCGTGGCGCGCTCGCGGCAAGCACTGGGATGGTGGTAACCTACCTCTGGAG	61
QY	787	aaccacaacgaagcccgccgaagctctgcagggccaactgactccagggccaacacagctctcat	846
Db	62	AACCCACACCCACCCACAGCCTTCAGAGCCACTGACCTCCATGGCAGCACACCCCTTCAT	121
QY	847	gcctctatgatagtcctgagacaattagctgagaaactgtgacaactgtgtgaccagatgat	906
Db	122	GCCTTAATGATGATCTGGAGCAACTCAAGCTCAAGTAATTCACATGGTAGGACACCATGAT	181
QY	907	gatyggctctctccaagcttggggccgagctctgcccctccgctgcaagcttgaggaatccgc	966
Db	182	GATGGCTCTCCCAAGCTGGGGCCCGCCTTGCCCTACGCTGCAAGCTTGAGCAATCCG	241
QY	967	aacctgaagatctcaagcctctgaagctgtgcgcgccaaggagggcaaatcgagaatttc	1026
Db	242	AACCTGAGAGATCTCAAGCCTCTGAACTTGACCTGGCCCAAGAGGGCAAGATCGAGATTTC	301
QY	1027	aggcacatccctgcagcggagattctcagaaactgagccaacctcccgaaagtccacggag	1086
Db	302	AGGCACATCTGAGGGGGGAGTTTTCAGAGCTAGCACACTTCCGAAAGTTCAACCGAG	361
QY	1087	tgtgtgcatatgggcctctgcgggtgtgcgctgtatgaaactgtgctctgtgcagactgtgag	1146
Db	362	TGGTGCTATGGGCTGTGCCGGGTGGCTGTAGACTGGCTTCTGTGGACACTGTGAG	421
QY	1147	gagaacacagctgtctgagatcatctgcttcatcttgcaagagcccgcaacgaaacggaatg	1206
Db	422	GAGACATCAATGCTGGAGATCATTTGCCCTTCATTCGAAGAGCCCGCAACCGACACCGAAAG	481
QY	1207	gtcgttttggagcccttgaaacaactgtctgcaggggaatggaatctgtctatccccaag	1266
Db	482	GTCGTGTGAGAGCCCTGAAACAAATGCTGCAGANGCAAAATGGGATGTGCTCATCTCTAAG	541
QY	1267	tctctcttaactctctgtatctagaactaaatttatctctacccgctgttgctac	1326
Db	542	GTCCTCTGAATCTCTGTGTATCTGATCTTACATTTCACTTCAACCCCTGGTGGCTAC	601
QY	1327	catcaagcctaacctgaagaagc-aggccgcccctccaccctgaaagcggaggtctggaactc	1385
Db	602	CATCACACTACTTGTAGAGAGCAAGGTGCTCCTCACTGAAAGCGGAGTT- GCAACTT	660
QY	1386	catgcgcgtgaagcggcacatc 1407	
Db	661	CATGCTGCTGACCGTGTCTATC 682	

RESULT	6		
BF940288/c			
LOCUS	BF940288	588 bp	EST
DEFINITION	7045f06..x1 NCI-CCAP Kid1 Homo sapiens cDNA clone IMAGE:3577090 3	22-JAN-2001	
	similar to TR:Q9Y5S1 Q9Y5S1 VANILLOID RECEPTOR-LIKE PROTEIN 1. ; ,		
	NRN sequence.		
ACCESSION	BF940288		
VERSION	BF940288.1	GI:12357608	
KEYWORDS	EST.		
SOURCE	human.		
ORGANISM	Homo sapiens		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		

REFERENCE 1 (bases 1 to 588)
 AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 JOURNAL Unpublished (1997)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
 Emmert-Buck, M.D., Ph.D.
 CDNA Library Preparation: M. Bento Soares, Ph.D.
 CDNA Library Arrayed by: Greg Lennon, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL, send email to:
 info@image.llnl.gov
 Seq primer: -400p from Glibco
 High quality sequence stop: 492.
 Location/Qualifiers
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 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:3577090"
 /clone_lib="NCI-CGAP_Kid11"
 /lab_host="DH10B"
 /note="Organ: Kidney; Vector: pT7T3D-Pac (Pharmacia) with
 a modified polylinker; Site_1: Not I; Site_2: Eco RI;
 Plasmid DNA from the normalized library NCI-CGAP_Kid3 was
 prepared, and ss circles were made in vitro. Following HAP
 purification, this DNA was used as tracer in a subtractive
 hybridization reaction. The driver was PCR-amplified cDNAs
 from a pool of 5,000 clones made from the same library
 (clonoids 1322376-1323911, 1456007-1456775, and
 1500552-1502855). Subtraction by Bento Soares and M.
 Fatima Bernaldo."
 BASE COUNT 110 a 173 c 163 g 142 t
 ORIGIN

Query Match 23.8%; Score 588; DB 171; Length 588;
 Best Local Similarity 100.0%; Pred. No. 2.4e-131;
 Matches 588; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

97 atgacctccctccagctctccagtttccaggttgaggacattgagtgaggaagcaaga 156
 |||||
 Db 588 ATGACCTCACCCTCCAGCTCTCCAGTTTCAGTTGAGACATGATGAGGCCAAGAA 529

97 gattgctctgagcgagagagaaagtgaatttggagcgagctgctcccatgag 216
 |||||
 Db 528 GATGGCTCGAGCGGACAGAGAAAGCTGATTTGGAGCGGCTGCTCCCATGGAG 469

217 tcaagttccagggcgagagaccggaattcgccctcagataagaagtcacactca 276
 |||||
 Db 466 TCACAGTTCCAGGCGGAGGACCGGAAATCGCCCTCAGATTAAGAGTCAACTCAAC 409

277 cgaagggagagaggggagcgagtgagccgagtcacaaacgattggaccgagatg 336
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 Db 408 CCAAGGGAACAGAGGTCGAGTCCGAGTCCAAACCGATTGGACCGAGATGGCTCTTC 349

337 aatggctcccgagggtgtcccgagagatctgctgagactccagagactgagcaag 396
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 Db 348 AATGGGCTGCCGGGGGTGTCCCGAGAGATCTGGCTGAGACTCCAGAGTACTGAGCA 289

397 accagaagttacatccagactcggataacagagagggctccagagtaagaagtgc 456
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 Db 288 ACCAGCAATACCTCAGCACTCGGAATACAGAGAGGGCTCAGAGTAAAGAGTGCCTG 229

457 atgaagagctgtctgaacttaagaagagagatgctgctgattctgcgaactgtc 516
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 Db 228 ATGAAGAGCTGTCTGAACCTTAAGAGAGGAGTCAATGCTGCTGCTGCTGCTGAG 169

517 atcgacagggactctgcaatccatcagccctgtaaatgtccagtgacagatactac 576
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 Db 168 ATCGACAGGAGTCTGGCAATCCTCAGCCCTGTAATGCCCATGTCAGACAGATAC 109

577 tacaggagccacagcgctctgcacalcgcacattgagaagagagtgctgagtg 636
 |||||
 Db 108 TACCGAGGCCACAGCGCTCTGCACATCGCCATGAGAAAGGAGTGTGCAGTGTGAG 49

637 ctcctgttgagagatggggccaatgagtcagcccgctgagccgc 684
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 Db 48 CTCCTGTGTGAGAGATGGGCGCAATGTGCAATGCCGGGCTGCGCGCGC 1

RESULT 7
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 LOCUS A1801897
 DEFINITION tx28h02.x1 NCI-CGAP Lu24 Homo sapiens cDNA clone IMAGE:2270931 3'
 similar to TR:035433 035433 VANILLOID RECEPTOR SUBTYPE 1. ;, mRNA
 sequence.
 ACCESSION A1801897
 VERSION A1801897.1 GI:5367369
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 616)
 NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
 Tumor Gene Index
 JOURNAL Unpublished (1997)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
 Emmert-Buck, M.D., Ph.D.
 CDNA Library Preparation: M. Bento Soares, Ph.D.
 CDNA Library Arrayed by: Greg Lennon, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 www.bio.llnl.gov/dbrrp/image/image.html
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 High quality sequence stop: 456.
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 /tissue_type="carcinoid"
 /lab_host="DH10B"
 /note="Organ: Lung; Vector: pT7T3D-Pac (Pharmacia) with a
 modified polylinker; Plasmid DNA from the normalized
 library NCI-CGAP_Lu5 was prepared, and ss circles were
 made in vitro. Following HAP purification, this DNA was
 used as tracer in a subtractive hybridization reaction.
 The driver was PCR-amplified cDNAs from a pool of 5,000
 clones made from the same library (clonoids
 141920-1417991 and 1520904-1522439). Subtraction by Bento
 Soares and M. Fatima Bernaldo."
 BASE COUNT 129 a 189 c 169 g 128 t 1 others
 ORIGIN

Query Match 23.4%; Score 578.4; DB 102; Length 616;
 Best Local Similarity 99.7%; Pred. No. 5e-129;
 Matches 579; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

97 1888 ttgagagctcttcaaatlcaacatcgagctggcgagctgctccacagagagctgac 1947
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 Db 616 TTGAGAGCTCTTCAAAATTCACATCGCATGGCGAGCTGGCTTCCAGAGAGAGCTGAC 557

97 1948 ttccggagcagagtgctctgctgtgctgctgagctgagctgctacactcctgct 2007
 |||||
 Db 556 TTCGGGAGAGTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 497

Oy	2008	cccaaatgctcatcgccccatgaagcggaaacggttaaacggttgcgcactgaaccttg	2067
Db	496	CTCCACATCTCTCATGCCCTTCATGAGCGAACCCTCAACAGTGTGGCCTGACAGACTGG	437
Oy	2066	agcattctggaagctcgagaagaagcacatctcttccttgaga tggagaatggttatgtg	2127
Db	436	AACATTCGTGAAGAGCTGCAGAAGCCATCTGTCTCTGAGATTGAGATTGGCTATTGTTGG	377
Oy	2128	tgcagagaagaagcagcaggcgaggtgtgatgtctgaccgtttggaactaaagccaagtgcagc	2187
Db	376	TGCAGAAACAACACAGCGGCGAGGTGTGATGCTCACCCGTTTGCCACTAAGCCAGATTGGCGCG	317
Oy	2188	cggagttgaagcgcgtgtgcttcaggggtgggggaaggtgaactgggcttcattatggagcgagc	2247
Db	316	CCGGATTGAGACGCTGGTGCTTCAGAGGTGAGAGAGGTAACTGGGCTTCATTGAGGACAGACG	257
Oy	2248	ctgcatacagctgtgtgaagaccggttaagggcaggtgtccctcgaactctgagaacct	2307
Db	256	CTGCCTACGCGCTGTGTGAGAGACCCGTCAGGAGGAGTGTCCTCTGAACTCTCGAAGACCT	197
Oy	2308	gtccctgtgtctcccctcccaaggagatgtgagatgtgtcctctgaagaaaactatgtgcc	2367
Db	196	GTCCTGGCTTCCTCCCTCCCAAGAGAGATGAGATGTCCTCTGAGAGAAAACZATTGTGGCCC	147
Oy	2368	gtccagagccctccatctccacatgacatggccccagatatgacagagagccagagacagaca	2427
Db	136	GTCCAGCTCTCTTCATTCACATGATGAGGCCCAATGACAGAGAGGCCAAGAGACAGCA	77
Oy	2428	gagagatcttccacaacacatctgtcgtcctgtggtgtccag	2468
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DEFINITION	602186482nt1 NIH_MGC_49 Homo sapiens cDNA clone IMAGE:4298445 3'		22-DEC-2000
ACCESSION	Bf690154		
VERSION	Bf690154.1		
KEYWORDS	GI:11975562		
SOURCE	EST.		
ORGANISM	human.		
REFERENCE	Homo sapiens		
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
JOURNAL	Mammalia; Euthera; Primates; Cetartia; Homalidae; Homo.		
COMMENT	NIH-MGC http://mgc.ncl.nih.gov/ National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999) Contact: Robert Strausberg, Ph.D. Email: cgabbs@email.nih.gov Tissue Procurement: ATCC/DCTP/DP CDNA Library Preparation: Ling Hong/Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: http://image.lnl.gov plate: LNCM154 row: C column: 22 high quality sequence start: 20 high quality sequence stop: 715. Location/Qualifiers 1. 984 /organism="Homo sapiens" /db_xref="taxon:9605" /clone_image="4298445" /clone_id="NIH_MGC_49" /lssue_type="melanotic melanoma, high MDR (cell line)" /lab_host="DH10B (phage-resistant)" /note="Organ: skin; Vector: pORF7; site_1: XhoI; site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor:		
FEATURES			
Source			

Query Match	Best Local Similarity	Matches 752: Conservative	Score 554;	DB 166;	Length 984;	Pred. No. 4,4e-123;	Mismatches 95;	Indels 21;	Gaps 12;
1606	gtgcgggctgctgtaacactgcttactactatgaacgttgctccagacaacaggactctac	1665	gGCACGAG(3). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH-MGC Library.	22.4%;	86.6%;	0;	284 g	203 t	200 a
893	gmgcttgccctgctgca-cttcttaacttaaccccttgctccagcactgacattgac	835							
1666	agtcgatgatccagaagtgatccctgcyggacactgtcgcctctctatcaactta	1725							
834	actgtcagagatccagaaatcatcccgcggaacctgtcgcggtccatctgattagag	775							
1726	gtctcccttcgcttcgtcgtctgag-ccctgtgagccttgagcagagagcttgag	1781							
774	tccttccttttcggcgttcgactgactgacccctgtgagctgagcccaaggagctttgg	715							
1782	caccgaag-----ctctacagagccccaatgccc--acagagtgatgagccatggag-9	1833							
714	gcgccacagacactccgcgtacagagccccaatgccaacagatcagtgacgcccatagag	655							
1834	ggacagagggagcagagggcaacggyggccagtagcagagggtatcctctgaaacctccttgag	1893							
654	ggacagaggaacgagggcgmacggggccacagacaggggtatctcggaagccctcttgag	595							
1894	ctct-ccaattcaacatcgcgcatggg-cgagcggygcctccagagagagctgaattcc	1951							
594	ctctgtcaaatcatcacatcgscatggctgacgtggccttcagagacagctgacattcc	535							
1952	ggcgcatgtgtcgtcgtctg-ctgcgtgactagtgctgtcactcaatcctgtctgc	2010							
534	ggcgcatgtgtcgtcgtctgctgctgctgctgacgtgacgtgacgtgacgtgacgtgac	475							
2011	aacatgtctacatcgccctcatgagagagacgttaaacagtgctgcacactgaagctgagc	2070							
474	aactgtctatcgccctcatgagagagacgttaaacagtgctgcacactgaagctgagc	415							
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414	attctggaagctgcagaaagccactcctgtctgtctgtcgtcgtcgtcgtcgtcgtcgtc	355							
2130	caggaagaag--cagcggygcaagtgatg-ctgacggttgcaactaagccagatgycag	2186							
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2187	cccggaatgagcgcgtggtgttcagagggggggggtgaactggtctcatagggagcagac	2246							
294	ccccgatgagcgttggtgttcagagggggagagtgtaactggtctcatagggagcagac	235							
2247	gtctgcacagcgtgtgtgagagaccgctaagggcaggtgtccctcgaactctgag-aac	2305							
234	gctgacctgacgtgtgtgagagaccgctaagggcaggtgtccctcgaactctgag-aac	175							
2306	ctgtctctgtgctccctcccaagagagatgagatggtgtcctctgagaaactatgtgc	2365							
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2366	ccgtccagcgtccctccagtgtaactgagagccagatgagcagagagggcagagagagag	2425							
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2426	cagaagatcttccaaccacatctgctg	2453							
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JOURNAL COMMENT

Unpublished (1997)
 Contact: Robert Strausberg, Ph.D.
 Email: cgabds-remail.nih.gov
 Oligo-dt track not found. Not a site shown in beginning of sequence is likely internal to the message. cDNA Library Preparation: M.B. Soares Lab Clone distribution: NCI-CGAP clone distribution
 Information can be found through the I.M.A.G.E. Consortium/LLNL at: www.bio.llnl.gov/dbp/image/image.html
 Seq primer: M13 forward
 POLYA-NO.

FEATURES

source

Location/Qualifiers

1..514

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE:2723216"

/clone.lib="NCI-CGAP_Sub3"

/lab_host="DH10B (Life Technologies)"

/note="Vector: pTZ19-Pac (Pharmacia) with a modified polylinker. Site 1: Not I; Site 2: Eco RI. The NCI-CGAP Sub3 library is a subtracted library derived from the NCI-CGAP Sub1 library, which is a subtracted library derived from B1. B1 constitutes a mixture of 21 normalized or subtracted NCI-CGAP libraries: NCI-CGAP_Co4, NCI-CGAP_P122, NCI-CGAP_P128, NCI-CGAP_Co10, NCI-CGAP_Co16, NCI-CGAP_P125, NCI-CGAP_Kid12, NCI-CGAP_Kid13, NCI-CGAP_Kid11, NCI-CGAP_Lym2, NCI-CGAP_Br23, NCI-CGAP_Co8, NCI-CGAP_C1L1, NCI-CGAP_Le12, NCI-CGAP_Lu19, NCI-CGAP_GC4, NCI-CGAP_GC6, NCI-CGAP_Br25. These 21 libraries were pooled and a single-stranded DNA preparation of the resulting mixture was used as a tracer in a subtractive hybridization with a driver whose composition is detailed below:

NCI-CGAP_Kid3 pool 1 LLM 3334-3337, 3682-3683, 3798-3803 (IMAGE Clonides 1322376-1323911, 1456008-1456775, 1500552-1502855); NCI-CGAP_Kid5 pool 1 LLM 3338-3342, 3722-3725, 3776-3778 (IMAGE Clonides 1323912-1325831, 1471368-1472903, 1492104-1493255); NCI-CGAP_Lu5 pool 1 LLM 3575-3582, 3851-3854 (IMAGE Clonides 1414920-1417991, 1520904-1522439); NCI-CGAP_GC4 pool 1 LLM 3164-3167, 3716-3720, 3733-3735 (IMAGE Clonides 1257096-1258631, 1465064-1470983, 1475592-1476743); NCI-CGAP_P122 pool 1 LLM 2457-2459, 2758-2759, 3062-3068 (IMAGE Clonides 985608-986759, 1101192-1101959, 1217928-1220615); NCI-CGAP_Co10 pool 1 LLM 2644-2653, 2871-2872 (IMAGE Clonides 1057416-1061255, 1144584-1145351). Subtraction was performed as previously described [Bonaldo, Lennon & Soares (1996) : Normalization and Subtraction: Two Approaches To Facilitate Gene Discovery. Genome Research 6, 791-806.

TAG_LIB=NCI-CGAP_Kid3
 TAG_TISSUE=Kidney
 TAG_SEQ=ATATGC

BASE COUNT 93 a 154 c 145 g 122 t
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Query Match 20.7%; Score 510.8; DB 113; Length 514;
 Best Local Similarity 99.6%; Pred. No. 1e-112;
 Matches 512; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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 290 gtgcagatcagccggaattcggaagcgaatcggtctcgaatcggtctcc 349
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QY 350 ggggtgtcccgagagatctggtctgagcttccagagctagtagcaagcagaatgacc 409
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 QY 410 tcaacgagcagagatcacagagagagtcacagagtagagtcctcgatgaagcgtgac 469
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 Db 214 tgaaccttaaggagagatgaatgacctgcatctgacacatgctgcagatgcagaagagact 155
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 QY 530 ctggagatctcagagccctggttaaatgcccagatgacagatgactattacagagccaca 589
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 Db 154 ctggagatctcagagccctggttaaatgcccagatgacagatgactattacagagccaca 95
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 QY 590 ggcgtgtgacatcgccatggaagagagatgagatggtgtgaaagccctgtgtgaga 619
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 Db 94 ggcgtgtgacatcgccatggaagagagatgagatggtgtgaaagccctgtgtgaga 35
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 QY 650 atggggccaatgtgcatgcccggcctgcgagccg 683
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 Db 34 atggggccaatgtgcatgcccggcctgcgagccg 1
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RESULT 13
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 similar to TR:035433 035433 VANILLOID RECEPTOR SUBTYPE 1. //, mRNA
 sequence.

ACCESSION AM467012
 VERSION AM467012
 KEYWORDS EST.
 SOURCE human.

ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 REFERENCE 1 (bases 1 to 512)
 AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index

JOURNAL COMMENT Unpublished (1997)
 CONTACT: Robert Strausberg, Ph.D.
 EMAIL: cgabds-remail.nih.gov
 TISSUE Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.
 CDNA Library Preparation: M. Bento Soares, Ph.D.
 CDNA Library Arrayed by: Greg Lennon, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
 www.bio.llnl.gov/dbp/image/image.html
 Seq primer: -400p from Gibco
 High quality sequence stop: 441.

FEATURES

source

1..512

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE:2873034"

/clone.lib="NCI-CGAP_Kid12"

/tissue_type="2 Pooled tumors (clear cell type)"

/lab_host="DH10B"

/note="Organ: Kidney; Vector: pTZ19-Pac (Pharmacia) with a modified polylinker. Site 1: Not I; Site 2: Eco RI; plasmid DNA from the normalized library NCI-CGAP_Kid5 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (clonides 1323912-1325831, 1471368-1472903 and 1492104-1493255). Subtraction by Bento Soares and M. Fatima Bonaldo."

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: October 4, 2001, 06:46:45 ; Search time 80.86 Seconds
(without alignments)
5780.474 Million cell updates/sec

Title: US-09-445-614-1

Perfect score: 2469
Sequence: 1 caccagagccgcagcgcagct.....gctgctctgggtccaccagt 2469

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 324599 seqs, 9465562 residues

Total number of hits satisfying chosen parameters: 649198

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Issued Patents, NA: *
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4: /cgn2_6/ptodata/1/lna/6B.COMB.seq: *
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6: /cgn2_6/ptodata/1/lna/6D.COMB.seq: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
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2	660.8	26.8	4803 4	US-09-197-636-1
3	660	26.7	4803 4	US-09-197-636-3
4	58.6	2.4	3489 2	US-08-728-333A-1
5	58.6	2.4	32207 2	US-08-770-379-20
6	58.6	2.4	32207 2	US-08-757-669A-20
7	55.2	2.2	1297 2	US-08-727-688-9
8	52.8	2.1	255 2	US-08-727-688-4
9	51.2	2.1	7218 1	US-08-232-453-14
10	48.4	2.0	1931 2	US-09-130-114-2
11	47	1.9	2580 3	US-09-050-863-2
12	47	1.9	3848 4	US-09-112-096-28
13	47	1.9	5452 2	US-09-130-114-1
14	47	1.9	5668 4	US-09-112-096-14
15	47	1.9	9600 4	US-08-910-647-1
16	47	1.9	10596 1	US-07-884-811-15
17	47	1.9	10596 1	US-07-885-971-15
18	47	1.9	10596 1	US-08-087-783A-15
19	47	1.9	10596 1	US-08-194-088B-15
20	47	1.9	10596 2	US-08-194-087-15
21	47	1.9	10596 3	PCT-US93-04648-15
22	46.2	1.9	16442 3	US-08-781-891-208
23	45.8	1.9	4252 3	US-08-475-844-4
24	45.8	1.9	4252 3	PCT-US95-08429-4
25	44.6	1.8	3924 5	US-08-726-214-9
26	44.2	1.8	2255 2	US-08-741-134-1
27	43.6	1.8	8202 1	US-08-258-420-13

28	43.2	1.7	900 5	PCT-US95-04801-3	Sequence 3, Appl
29	43	1.7	9515 1	US-08-920-812-13	Sequence 13, Appl
30	43	1.7	9515 1	US-08-920-827-13	Sequence 13, Appl
31	43	1.7	9515 1	US-08-921-177-13	Sequence 13, Appl
32	43	1.7	9515 1	US-08-362-577C-13	Sequence 13, Appl
33	43	1.7	9515 2	US-08-920-828-13	Sequence 13, Appl
34	42.2	1.7	6363 2	US-08-929-967-6	Sequence 6, Appl
35	41.2	1.7	1995 1	US-08-425-069-3	Sequence 3, Appl
36	41.2	1.7	1995 2	US-08-317-844B-3	Sequence 3, Appl
37	41	1.7	2326 2	US-08-231-193A-41	Sequence 41, Appl
38	41	1.7	2326 2	US-08-486-273A-41	Sequence 41, Appl
39	41	1.7	2326 3	US-08-480-474-41	Sequence 41, Appl
40	41	1.7	2326 3	US-08-940-086A-41	Sequence 41, Appl
41	41	1.7	3243 2	US-08-231-193A-44	Sequence 44, Appl
42	41	1.7	3243 2	US-08-486-273A-44	Sequence 44, Appl
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44	41	1.7	3243 3	US-08-940-086A-44	Sequence 44, Appl
45	41	1.7	3698 2	US-08-231-193A-43	Sequence 43, Appl

ALIGNMENTS

RESULT 1
US-09-197-636-7
Sequence 7, Application US/09197636
Patent No. 6239267
GENERAL INFORMATION:
APPLICANT: DICKMORTH, DAVID
APPLICANT: HAYES, PHILIP
APPLICANT: MEADOWS, HELEN
APPLICANT: DAVIS, JOHN
TITLE OF INVENTION: NOVEL COMPOUNDS
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ratner & Prestia
STREET: P.O. Box 980
CITY: Valley Forge
STATE: PA
COUNTRY: US
ZIP: 19482-0980
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/197,636
FILING DATE: 23-NOV-1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: UK 9805137.8
FILING DATE: 12-MAR-1998
APPLICATION NUMBER: UK 9815791.0
FILING DATE: 21-JUL-1998
APPLICATION NUMBER: UK 9819278.4
FILING DATE: 03-SEP-1998
ATTORNEY/AGENT INFORMATION:
NAME: Prestia, Paul F
REGISTRATION NUMBER: 23,031
REFERENCE/DOCKET NUMBER: GP-30075
TELECOMMUNICATION INFORMATION:
TELEPHONE: 601-407-0700
TELEFAX: 610-407-0701
TELEX: 846169
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 3500 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-09-197-636-7

Query Match	26.8%;	Score 660.8;	DB 4;	Length 3500;
Best Local Similarity	61.1%;	Pred. No. 3.7e-151;		
Matches 1206;	Conservative 0;	Mismatches 732;	Indels 36;	Gaps 7;

OY	316	tttaaccgaagtcgtgcctccaatctgctgtctcccggtgtgtcccggaagatctgtcgtga	375
Db	1200	TATGATCCAGGAATATCTTTGAAGCCGTGTGCTCAAAATTAAGTCCAGGATTTGGAGAC	1255
OY	376	cttccagatcactcgtgagcaagaccagcaaatatcctaccgaactcgtgaatatacagaggc	435
Db	1260	CTGCTGCTTCTCGGAGAAAGCAGAAACACACTCTACAGACAAACGATTCAAAAGACCT	1319
OY	436	tcacaaagttaagacgtgtcctgtatgtgaaggtctgtcctaaaccttaaggaacgtatcgtcc	495
Db	1320	GAGACAGGGAAGACCTCTCTGCTGAAGAACCATCTCAACTGTGACACACGACAGAAACAC	1379
OY	496	tgcaatctgcgaactcgtgcgaagatcgaaggagactcgtggaatctcgaacctgaacctgttaat	555
Db	1380	ACCATTCCTCCCTGCTCTCTGGAGATGTGGCGGCACACGACAGCCTGAAGGATTTGTCAAC	1439
OY	556	gcccagatgcacagaatgaactatlaaccagagccacagcgtctctacatgcatactgaagaag	615
Db	1440	GCCAGCTACAGGACGACACTCTACAAAGGGCCACAGACACTGCATCTGCCATTCGAGGA	1499
OY	616	aggagctctgcaggtctgtgtgaaggtctcctgtgtgagaatctgggtccaatgtcatgtccgggtc	675
Db	1500	CGAACAATGGCCTGTGTGACCTCTGCTGTGAAGAGGAGACAGAGCTCCAGGCTCGGCC	1559
OY	676	tgccgcgcgtctctccacgaagggccaaag---ggactgtcttaattctgtgtgaatacc	732
Db	1560	CATGGGGACTTCTTTAGAAACCAACAAAGGGCGGCTCGGATTCTACTCGGTAACTGGCC	1619
OY	733	ctctctcttgccgcgtctgcacaaagcagtggatgtgtgaagtactacctctctgtagaacca	792
Db	1620	CTGTCCCTGGCGCGGTGTCACCAACAGCTGGCGATGTGAATGTTCTGCTGCAGAACTCC	1679
OY	793	caccagcccgccagccgtcgaagggccactgtactcccaaggaaacaacgtctgtatgtcccta	852
Db	1680	TGGCAGACGGCCGACATCAACGCCAAGGAGATCTGCTGGGACACGCTGTGTGCACCCCTG	1739
OY	853	gtgaatgctcgtgacaactcgtacgtctgaaacatgtcacgtgtgtaccagcatgtatgtggt	912
Db	1740	GTGAGAGTGGCGGCACACACAGCGCCGACAAACAGAAATTGTGTACGAGATGTACATATAG	1799
OY	913	ctctctccaagctgtgggtccgcctctgtccctacgtgtgacgttgaggaatcccgaaactgt	972
Db	1800	ATTCTGTATCTGTGGGGGCAAACTGCACCCGACGCTGTAACTGTGAAGAGCTCCACCAACAG	1859
OY	973	caggatctcagcgtctcgtgaagctgtgscgcgcgaaggtggaagatatgaaatttcaagaac	1032
Db	1860	AAGGGAATGACGCCGCTGCTCTGGCAGCTGGGACCGGGAATGTGGGTCTTGCCCTAT	1919
OY	1033	atcctcgaagcgtggagatt-----ttcaagactgtgagccacttcccgaaagtctacagag	1086
Db	1920	ATTCTCAAGGGGAGATTCACGAGAGCCGAGTGGAGGCACTGTCCAGGAAGTTACAGAG	1979
OY	1087	tggtgtcatatgtggcctgtcgcggtgtgtcgtctgtatgacctgtgtctgtgtgaacgtgtgag	1146
Db	1980	TGGGGCTTACGGGGCCGTGTGCACTCTCTGCTGTACGACATGTCTCTGCATGACACCTGGCAG	2039
OY	1147	gagaaectcagttctgtgagatcatctgtcttcaatctga---agaagccgcacgcgaacacga	1203
Db	2040	AAGAACTCGGTCTGGAGGTGATCGCTTACACAGCAGCAGGAGACCCCTTAATGTGGCACAC	2099
OY	1204	atgtgtcttttggagcccttgaacaaactcgtgtcaggtcgaaattgtga---tctgtcatc	1260
Db	2100	ATGCTTGTGTGAGCGCGGTGAACCGAATCTCGAGAGCAAGATGGGACAAATTTGTGTAG	2159
OY	1261	cccaagttctctttaaactctctgtgtatactgcatactacaagtctaatcttcaacgcgtgt	1320
Db	2160	CGCATCTTACTTCAACTCTCTCGGTCTATGCTCGCTGTACATGATATATTTACCATGGCT	2219

OY	1321	gcaccatcaagccttaaccctgaagaagcaagccgcgcctccacactgaagcggaggtctgga	1380
Db	2220	GCCTTACTACAGGCC-----CGTGGATGGCTTCCTCCCTCTTTAAATGGAATAAATCGGA	2273
OY	1381	aactcatalgctgctgacggcgccacatccatctatccctctgaaggggatctacctctgtg	1440
Db	2274	GACTATTTCGAGATTACTGAGAGATCCGTGTCTGTGTTAGGAGAGTCTACTCTTTTTC	2333
OY	1441	ggccagctgtgtaactctgtgcggcgccagcgtgtcaatctgatctgtlctaaagacac	1500
Db	2334	CGAGGGATTGATATTTCCTGCGACAGAGCGCGCTCATGAAGACCCTGTTGTGACAGC	2393
OY	1501	tactttaaatctctctctgcttcacggccctgctctaacgctgtgtgccaggtctgtgt	1560
Db	2384	TACAGTAGATAGCTTTCTTTCTTCTGACAGTACCTGTTATGCTGTGACCGGTGGTGTGAC	2453
OY	1561	tctctggccatcgagtgtgtaacctgcccctgctgtgtctcgtgcgtgtgtcgtgcgtgtg	1620
Db	2454	TTCAAGCACCCTCAAGAGATATGTGGCTTCCATATGATATTCCTCTG6CCTTG6GCTG6AC	2513
OY	1621	aaactgcttaactatacaacgttgcttcacagcacacagggcatctacagttcatcacag	1680
Db	2514	AACATGCTCTACATACACCCCGGGTTTCCAGAGATGGGATGTATGCGGTATGATAG	2573
OY	1681	aagtaactcctggaggaaacctgctgcgctctctctctgatatctaatgtcttcccttggc	1740
Db	2574	AAGATGATCCTGAGAGACCTGCTCCCTTTCAATGTTGTCTAGTGCTGTCTTGTGCGG	2633
OY	1741	tctccttaagccctgtgtgagcctcgaaacagaggagctgtgcgcccgaagctccataacgc	1800
Db	2634	TTTTCCACACCGGTGGTGAAGCTGATTTGAAGACGGGAAGATGATCCTCCTCGCTGAG	2693
OY	1801	cccaatgccacagatcaagtgcagcccatgtgagggagcaggaagacgaaggcaacggggcc	1860
Db	2694	TCCACGTC-----GCACAGATGGCGGGGGCCCTCGACAGGCCCCCGATAGC	2741
OY	1861	cagtaacggggatctcctgtaagagctctctctggagctcttcaatctaccatctgcatgggc	1920
Db	2742	TCTTACACACGCTGTACTTCCACTCTCCGAGGCTGTTCAAGTTACCATGGCATGGGC	2801
OY	1921	gagctgagccttccaggaagcagctgtcaccttcgcggcgcatgtgtctgtctgtctgtgcc	1980
Db	2802	GACCTGAGTTCACTAGAAATATGACTTCAAGGCGTCTTATCATCTCTCTGCTGGCC	2861
OY	1981	taagtctgtcctaaccatacctctgtcgtcctaaatgtctcatcgcctctcatgagcgagacc	2040
Db	2862	TATGTATTCTCACTACATCTCCTCCGCTCAACATGCTCATGCGCCTCATGGGAGAGCT	2921
OY	2041	gtcaaacgvtgtgcacactgacagctgtgagcatcttgaaagctgtgcgaagaagccatctctgtc	2100
Db	2922	GTCAACACAGATCCACAGAGAGCAAGAACATCTGGAAGCTGCACAGAGCCATACATC	2981
OY	2101	ctggaagatgtaagaatgtgcatactgtgtgtcagaagaag-----cagcgggcgaggtgtatg	2157
Db	2982	CTGGAACCGSAGAAAGCTTCTTAAGTGATGAGAGAAAGGCTTCGCTCAAGGCACACTG	3041
OY	2158	ctgaacgctgtgacataagccagatgtgcagcccggaatgaacgctgtgtgtcttaaggtgtgag	2217
Db	3042	CTGCAAGTGGGATACACACTGATGGCAAGAGACACTACCGGTGTGCTTCAAGGTGAGC	3101
OY	2218	gaaggtgaactcgggtctcatgtgtgagcagagcgtgtcctaagctgtgtgtgagaccgg	2271
Db	3102	GAGTGAATCTGAGCAACCTGGAACACCAACGTGGGCAATCATCAACGAAGACCCG	3155

RESULT 2
US-09-197-636-1
Sequence 1, Application US/09197636
Patent No. 6239267
GENERAL INFORMATION:
APPLICANT: DUCKWORTH, DAVID
APPLICANT: HAYES, PHILIP

APPLICANT: MEADOWS, HELEN
 APPLICANT: DAVIS, JOHN
 TITLE OF INVENTION: NOVEL COMPOUNDS
 NUMBER OF SEQUENCES: 8
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Ratner & Prestia
 STREET: P.O. Box 980
 CITY: Valley Forge
 STATE: PA
 COUNTRY: US
 ZIP: 19482-0980
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FastSeq for Windows Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/197,636
 FILING DATE: 23-NOV-1998
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: UK 9805137.8
 FILING DATE: 12-MAR-1998
 APPLICATION NUMBER: UK 9815791.0
 FILING DATE: 21-JUL-1998
 APPLICATION NUMBER: UK 9819278.4
 FILING DATE: 03-SEP-1998
 ATTORNEY/AGENT INFORMATION:
 NAME: Prestia, Paul F.
 REGISTRATION NUMBER: 23,031
 REFERENCE/DOCKET NUMBER: GP-30075
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 601-407-0700
 TELEFAX: 610-407-0701
 TELEX: 846169
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 4803 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 US-09-197-636-1

Query Match 26.8%; Score 660.8; DB 4; Length 4803;
 Best Local Similarity 61.1%; Pred. No. 4.2e-151;
 Matches 1206; Conserved: 0; Mismatches: 732; Indels 36; Gaps 7;

QY 676 tggcgccgtcttccagaagggccaag---ggacttgctttatttggtgagctacc 732
 DB 1560 CATGGGAGACTCTTTAAAGAAAACAAAGGCGCGCTGGATTTACTGCTGATGAGCC 1619
 QY 733 cctcttggccgttgcacaaagagtggtgagtaagctactccttgagaacca 792
 DB 1620 CTGTCCCTGGCCGCTGACCAACCAAGCTGGGATGTAAGTCTCTGTGCAACATCC 1679
 QY 793 caccagcccgccagcctgcgaagcactgcctccagggcaacacagctcctgacctta 852
 DB 1680 TGGCAGAGGCGCCGACATCAGCGCCAGGAGACTGGGGGCAACACGTTGCTGACCCCTG 1739
 QY 853 gtgatgatcggaaacactcagctgagaacattgactgtgtgaccagcaatgataaggg 912
 DB 1740 GTGGAGGTGGCCGACAAACGCGCCGCAACAGAAATTGTGACAGCATGTACATGAG 1799
 QY 913 ctccccaagctggggggccgctctgccttaccgtgagcgttgagaaatccgaaacctg 972
 DB 1800 ATTCTGATCTGGGGGCCAAACTGCACCCGACGTGAAGCTGGAGAGCTCACCAACAG 1859
 QY 973 caggatctcagcctctgaagctggccgcgaagggaggaatcgaatttcaaggcac 1032
 DB 1860 AAGGGAATACCCCGCTGGCTGTGGCAGCTGGAGACCGGGAATGGGCTCTTGGCTTAT 1919
 QY 1033 atccctgcagcgggagtt-----ttcaggactgagccacattcccgaaagttcacagg 1086
 DB 1920 ATTCTCAGCGGAGATTCAGAGAGCCGAGTGCAGACACTCTCCAGAAATTCACCGAG 1979
 QY 1087 tggctctatggcctgctcggagtgctcgctgtatgacctggtctctgtgagcagctgtgag 1146
 DB 1980 TGGGGCTTAGGGCCCGGTGACTCTCGCTGACACCTGCTGATGATGACACTGCGCAG 2039
 QY 1147 ggaactcagctgtgagaatcattgcttcaatca---agaagccggacagcaacaga 1203
 DB 2040 AAGAACTCGTCTGAGAGTATCGCTTACAGCAGCAGGAACCCCTTATGCCACGAC 2099
 QY 1204 atgttgcttggagcccttgaaacaaactctgcagggcgaattggga---tctgtcattc 1260
 DB 2100 ATGCTTGTGGAGACCGCTGAACCGACTCTGACGAGCAAGTGGAGAGATTCGTCAAG 2159
 QY 1261 cccaagttctttaaactcctctgtgtaactcgtactaataatgttacttaccgctgtt 1320
 DB 2160 CGCATCTTCTACTTAACCTCTGCTGTACTGCTGATATCATCATCTTCCATCGGT 2219
 QY 1321 gctacacatcagcctacacctgagaagcagcgcccccacactgaagcggaggttga 1380
 DB 2220 GCTTACTACAGCC-----CGTGAATGGCTTGCTCTTAAATGGAATAAACTGGA 2273
 QY 1381 aactccatgtctgtcagggccacacacttcttctgtcgttaggggagatcactcctgtg 1440
 DB 2274 GACTATTTCGAGTACTGAGAGATCCGTCTGTGTTAGAGAGATCTACTTTTTC 2333
 QY 1441 ggcacgtgtgttacttctgcggcgccagcagtggtcattcgtatcgttataaagc 1500
 DB 2334 CGAGGATTCATATTCTCTGAGAGGCGCGCTGATGATMAACCTCTTGTGACAGC 2393
 QY 1501 tactttgaatcctcttctcgtgttcacagggccgtgcacagtggtgtcccaagtgctgt 1560
 DB 2394 TACAGTGAATCTTTCTTCTGTGCACTACGTTCATCTGCGCACCGTGTGCTGTAC 2453
 QY 1561 ttcctgccaatcagtgtaactcgtccctctgtgtctgcgtggtgtgctgtgctg 1620
 DB 2454 TTCACGCCACCTCAAGAGATGTGCTTCCATGATATTCCTCGGCTGGCGTGGAGAC 2513
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 DB 2514 AACATGCTCTACTACACCGCGGTTTCCAGCATGGGATTAAGCCGTGATGAAG 2573
 QY 1681 aaggtaactcgtcggagcctgtcgtcctcctcgtatcactaattagcttctcttcggc 1740
 DB 2574 AAGATGATCTCTAGAGACTGTGCGGTTTCACTTGTGTATATGCTCTTGTGTCGGG 2633
 QY 1741 ttcgctgttagccctgtgagcctgagcaggagcgttggcgcccggaagcctctcaaggc 1800

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Db 2634 TTTTCACAGCGGTGTGACGCTGATTTGAAGAGGAGATGACTCCTGCGGTGTAG 2693
QY 1801 cccaatgacagagatcagtgacagccatgagaggaacagaggaacagagagcc 1860
Db 2694 TCCAGGTC-----GCACAGGTGGCGGGGGCCCTGAGAGGCCCCCGATAC 2741
QY 1861 cagtaacagagatccttggaagcctccttgagctcttaaatlaacatcgagatggc 1920
Db 2742 TCCACACAGAGGCTTACTCCACCTGCTGAGCTGTTCAAGTTCAACATCGGATGGCC 2801
QY 1921 gagctggcctccagagcaagctgacatcccgagcatggtgctgctgctgagcc 1980
Db 2802 GACCTGGAGTTCACTGAGAACTATGACTTCAAGGCTGTCTTATATCTGCTGCTGCTG 2861
QY 1981 tacgtgctcactacatactctgctgctcaaatgctcaatgctcaatgagagagcc 2040
Db 2862 TATGTAATCTCCTTACTTACTCTCTCTCTCAACATGCTCATGCGCTCATGGGTGAGCT 2921
QY 2041 gtcaacagtgctcactgacagctgagcatctggaagctgagcaagagccatctctc 2100
Db 2922 GTCAACAGATCGACAGAGAGAGAGAAACATCTGGAAGCTGCAAGAGCCATCACCATC 2981
QY 2101 ctggaagatggaatggtatggtggtggtggtggtggtggtggtggtggtggtggt 2157
Db 2982 CTGACACAGGAGAGAGAGCTTCTTAAGTCATGAGGAGAGAGAGAGAGAGAGAGAG 3041
QY 2158 ctgagcgtgctcactaagcaagatgagagagagagagagagagagagagagagag 2217
Db 3042 CTGACAGGTGGGTACACACCTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3101
QY 2218 gaggtgagctgagctcagtgagagagagagagagagagagagagagagagagag 2271
Db 3102 GAGGTGAACGTGAGACCACTGTGAGACCAAGCTGGGCTATCAACAGAGAGAGAG 3155

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RESULT 3

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US-09-197-636-3.
Sequence 3, Application US/09197636
Patent No. 6239267

```

GENERAL INFORMATION:

```

APPLICANT: DUCKWORTH, DAVID
APPLICANT: HAYES, PHILIP
APPLICANT: MEADOWS, HELEN
APPLICANT: DAVIS, JOHN
TITLE OF INVENTION: NOVEL COMPOUNDS
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESS: Ratner & Prestia
STREET: P.O. Box 980
CITY: Valley Forge
STATE: PA
COUNTRY: US
ZIP: 19482-0980

```

```

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/197,636
FILING DATE: 23-NOV-1998
CLASSIFICATION:

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PRIOR APPLICATION DATA:
APPLICATION NUMBER: UK 9805137.8
FILING DATE: 12-MAR-1998
APPLICATION NUMBER: UK 9815791.0
FILING DATE: 21-JUL-1998
APPLICATION NUMBER: UK 9819278.4
FILING DATE: 03-SEP-1998
ATTORNEY/AGENT INFORMATION:
NAME: Prestia, Paul F
REGISTRATION NUMBER: 23,031

```

```

REFERENCE/DOCKET NUMBER: GP-30075
TELECOMMUNICATION INFORMATION:
TELEPHONE: 601-407-0700
TELEFAX: 610-407-0701
TELEX: 846169
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 4803 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-09-197-636-3

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Query Match 26.7%; Score 660; DB 4; Length 4803;
Best Local Similarity 61.0%; Pred. No. 6,5e-151;
Matches 1204; Conservative 2; Mismatches 732; Indels 36; Gaps 7;

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QY 316 ttgacagagatcggctctcaatgagctgctcggggtgtcccgagagatcgtgtga 375
Db 1200 TATGATCGAGAGATATCTTTGAAGCCGTTGCTCAAAATACCTGCGAGATCGAGAGC 1259
QY 376 ctccaagatcactgaagacacagcaagtaacctcaccgactcggatatacagagagcc 435
Db 1260 CTGCTGCTCTTCTCTCAAGAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 1319
QY 436 tccaagtgagagtgctgctgagagagctgctgagagagagagagagagagagagag 495
Db 1320 GAGAGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1379
QY 496 tgcattctgcaactgctcagatgagagagagagagagagagagagagagagagagag 555
Db 1380 ACCATCCCTCCCTGCTCTGAGATGCGCGGCAAGGAGAGAGAGAGAGAGAGAGAGAG 1439
QY 556 gccacagtgacagatgacatataccagagagagagagagagagagagagagagagag 615
Db 1440 GCCRGCTACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1499
QY 616 agagatctgacgtgtgagagctcctggtgagagagagagagagagagagagagagag 675
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QY 732 ctctcttgagcgtctgacacagagagagagagagagagagagagagagagagagagag 792
Db 1620 CTGTCCTGCGCGGCTGACCAACCACTGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1679
QY 792 caccagccgagcagctgagagagagagagagagagagagagagagagagagagagagag 852
Db 1680 TGCCACAGCGCCGACATCAACGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1739
QY 852 gtgatgctcagagagagagagagagagagagagagagagagagagagagagagagag 912
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QY 912 ctctcccaagctlgggccgagcctcctcagcagctgagagagagagagagagagagag 972
Db 1800 ATTCTGATCTTGGGGCCAAACTGCAACCGACCTGAAGCTGAGAGAGAGAGAGAGAG 1859
QY 972 cagagatcagagccttgaagctgagcagagagagagagagagagagagagagagagag 1032
Db 1860 AAGGGAATGACCGCGCTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1099
QY 1032 atccctcagagagagagagagagagagagagagagagagagagagagagagagagag 1086
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 Qy 1147 gagaactcaatgtctgagatcatctgtcttcatltyca---agagcccgacagaccca 1203
 Db 2040 AAGAACTCGGCGTGGAGGATGATGCGCTACAGCAGCAGCAGACCCCAATCGCACAC 2099
 Qy 1204 atgtgtcttcttgagcccttgacaaactctgacagcgaaatgga---ctctgcatc 1260
 Db 2100 ATGCTCTTGGTGGAGCGCGTGAACCGACTCCTGACGAGCAAGTGGACAGATTCGTCAG 2159
 Qy 1261 ccaagttcttctaactctctgtgaatctgatactgatactgatactgatactgatact 1320
 Db 2160 CGCATCTTCTACACTTCACTCTCTGCTACTGCTGATGATGATGATGATGATGATGAT 2219
 Qy 1321 gctacacatcagccctacacccctgaagaagcagcgccctcaccctgaagcgaggttga 1380
 Db 2220 GCGTACACAGAGCC-----CGTGGATGGCTTGGCTCCTCTTAAGATGGAAGAAAACTGA 2273
 Qy 1381 aactcactgtctgacagcgacacatccttactctgtagggaggtactactctctgtg 1440
 Db 2274 GACTATTTCCGAGTACTGAGAGATCTCTGTGTAGAGAGAGTCTACTCTTTTTC 2333
 Qy 1441 ggcacgtctgtactctctgtgagcgccagcgtgtcactctgactctgactatagacgc 1500
 Db 2334 CGAGGGATTCAGTATTTCTGACAGAGCGCGCTGATGATGAAGACCTGTTGTGACAGC 2393
 Qy 1501 tacttgaatccct 1560
 Db 2394 TACAGTGAAGTGTCTTCTTCTTCTGACAGTCTGATGATGATGATGATGATGATGAT 2453
 Qy 1561 tctctgacatcagagtgtagctgacccctctgtctgtctgtctgtctgtctgtctgt 1620
 Db 2454 TTTCAGCAGCTTCAAGAGATGATGCTTCCATGCTATCTCTCTGCGCTTGGCGTGGAGC 2513
 Qy 1621 aacctgttactactaactgtagtctgtagcagacagcagcagcagcagcagcagcagcag 1680
 Db 2514 AACATGCTTACTACTACCCCGGCTTCCAGAGAGAGGACATGATGCGTATGATGATGAT 2573
 Qy 1681 aagctcatctctgagacccctgtctgtctctctctctctctctctctctctctctctct 1740
 Db 2574 AAGATGATCTCGAAGACCTGTGCGCTTCAATGTTGTCTCAATGCTGTTCTTGTTCGG 2633
 Qy 1741 tctgtctgacccctgtgtgagcctgagcagagagctgtgagcccgacagctcctacagc 1800
 Db 2634 TTTCCTCAGAGGCTGAGCCTGATGATGATGATGATGATGATGATGATGATGATGAT 2693
 Qy 1801 cccaatgcccacagagtagtgcagcccatgagagagagagagagagagagagagagag 1860
 Db 2694 TCCACGTC-----GCACAGTGGCGGGGCGCTGCTGAGGCCCCCGATAGC 2741
 Qy 1861 cagtagcaggggtagctcagagacccctctgtgagctcttcaaatcaccatcagcagcagc 1920
 Db 2742 TCCGACAAAGCCCTGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2801
 Qy 1921 gagctgacctcagagagagcagctgcaacttcgagcagcagcagcagcagcagcagcagc 1980
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 Db 2862 TATGTATTTCTCACTCTCACT 2921
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 Db 2922 GTCAACAAGATCCGACAGAGAGAGCAAGATCTGGAAGCTGCAAGAGCATCATCATCATC 2981
 Qy 2101 ctggaagctggaagagctatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 2157
 Db 2982 CTGACACCGAG 3041
 Qy 2158 ctgacagctggaag 2217
 Db 3042 CTGACAGTGGGCTGACACCTGATGATGATGATGATGATGATGATGATGATGATGATG 3101

Qy 2218 gaggtagaactgggtct 2271
 Db 3102 GAGCTGAAGTGGAGACCACTGACACCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3155

 RESULT 4
 US-08-728-323A-1/c
 : Sequence 1, Application US/08728323A
 : Patent No. 5948676
 :
 : GENERAL INFORMATION:
 : APPLICANT: Chang, Yuan
 : APPLICANT: Bohenzky, Roy A.
 : APPLICANT: Russo, James J.
 : APPLICANT: Edelman, Isidore S.
 : APPLICANT: Moore, Patrick S.
 : TITLE OF INVENTION: Immediate Early Protein From Kaposi's
 : TITLE OF INVENTION: Sarcoma-Associated Herpesvirus, DNA
 : NUMBER OF SEQUENCES: 21
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: Cooper & Dunham LLP
 : STREET: 1185 Avenue of the Americas
 : CITY: New York
 : STATE: New York
 : COUNTRY: U.S.A.
 : ZIP: 10036
 :
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: Floppy disk
 : COMPUTER: IBM PC compatible
 : OPERATING SYSTEM: PC-DOS/MS-DOS
 : SOFTWARE: Patentin Release #1.0, Version #1.30
 : CURRENT APPLICATION DATA:
 : APPLICATION NUMBER: US/08/728,323A
 : FILING DATE:
 : CLASSIFICATION: 435
 : ATTORNEY/AGENT INFORMATION:
 : NAME: White, John P.
 : REGISTRATION NUMBER: 28,678
 : REFERENCE/DOCKET NUMBER: 0575/52268/JPM/MS/SKS
 : TELECOMMUNICATION INFORMATION:
 : TELEPHONE: 212-278-0400
 : TELEFAX: 212-391-0525
 : INFORMATION FOR SEQ ID NO: 1:
 : SEQUENCE CHARACTERISTICS:
 : LENGTH: 3489 base pairs
 : TYPE: nucleic acid
 : STRANDEDNESS: single
 : TOPOLOGY: linear
 : MOLECULE TYPE: DNA (genomic)
 : FEATURE:
 : NAME/KEY: CDS
 : LOCATION: 1..3489
 : US-08-728-323A-1

 Query Match 2.4%; Score 58.6; DB 2; Length 3489;
 Best Local Similarity 47.0%; Pred. No. 4.5e-05;
 Matches 181; Conservative 0; Mismatches 204; Indels 0; Gaps 0;

1386 catgctgtgacgagccacatccttatacctgttaggggagatctacccctcgtgcca 1445

[illegible]

RESULT 7
 US-08-727-688-9
 Sequence 9, Application US/08/27688
 Patent No. 5919638
 GENERAL INFORMATION:
 APPLICANT: Russell, John C.
 TITLE OF INVENTION: Reagents and Methods for Detecting Prostate Tumors
 NUMBER OF SEQUENCES: 36
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Abbott Laboratories
 STREET: 100 Abbott Park Road D377/APED
 CITY: Abbott Park
 STATE: IL
 COUNTRY: USA
 ZIP: 60064
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FastSeq Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/727,688
 FILING DATE:
 CLASSIFICATION: 514
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER:
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Porembski, Priscilla E.
 REGISTRATION NUMBER: 33,207
 REFERENCE/DOCKET NUMBER: 5967. US. 01
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (847) 937-0378
 TELEFAX: (847) 938-2623
 TELEX:
 INFORMATION FOR SEQ ID NO: 9:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1297 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 IS-08-727-688-9

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Best Local Similarity 56.7%; Pred. No. 0.00021;
Matches 102; Conservative 0; Mismatches 70; Indels 0; Gaps 0;

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 Db 511 GGGCCAGGGGGGCGACCGGCTCTCCAGTAGCAACTGGCGGGGAGTCTCTCTCGT 590
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RESULT      8
US-08-727-688-4
; Sequence 4, Application US/08727688
; Patent No. 5919638
; GENERAL INFORMATION:
; APPLICANT: Russell, John C.
; TITLE OF INVENTION: Reagents and Methods for Detecting Prostate Tumors
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Abbott Laboratories
; STREET: 100 Abbott Park Road D577/AP6D
; CITY: Abbott Park
; STATE: IL
; COUNTRY: USA
; ZIP: 60064
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/727,688
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Porembski, Priscilla E.
; REGISTRATION NUMBER: 33,207
; REFERENCE/DOCKET NUMBER: 5967.US.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (847) 937-0378
; TELEFAX: (847) 938-2623
; TELEX:
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 255 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
US-08-727-688-4

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Best Local Similarity 57.1%; Pred. No. 0.00045;
Matches 96; Conservative 0; Mismatches 72; Indels 0; Gaps 0;

QY 1917 gggcgagctggtcctccagcagcagctgcacctccggcgagatggtgctgctgctgct 1976
Db 79 GGGCCAGCGGGGACACCTCGTCCCACTATGCCAATCGCGTGGGGTGGTCTGCTCGT 138

QY 1977 ggcctacgtgctgcctcacctacatcctgctgctcaaatgctctacggccctcagagga 2036
Db 139 CATCTCTCTCTGCTCGGGCCACACATCTCTCTGCTACACTGCTCTCATTTGCCATGTTCA 198

QY 2037 gaccgtcaacagltgcgcacactgaacagcttgagacatctggaagtgcga 2084

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Db 703 cgtctctcgtctctcccgctctctcgtctctcccgctctcgtctctcccgctctcccgctctcc 762
 Oy 1911 cggcagtcggcgagctcgtgccttcaggaagcagctgcacctccggaggaatgctcctcct 1970
 Db 763 cgtctctcccgctctcccgctctcgtctctcccgctctcccgctctcgtctctctcc 822
 Oy 1971 gctcgtgcctacgtctgcttgcacacatcgtctcgtccaaacatctacgtcc 2028
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RESULT 11

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US-09-050-863-2/c
Sequence 2, Application US/09050863
Patent No. 611411
GENERAL INFORMATION:
APPLICANT: LAO, Ying
APPLICANT: Hiang, Betty
APPLICANT: Payan, Don
TITLE OF INVENTION: Mammalian Protein Interaction Cloning
TITLE OF INVENTION: System
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fleury, Hobbach, Test, Albritton & Herbert
STREET: 4 Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94111-4187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/050,863
FILING DATE: 30-MAR-1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Silva, Robin M.
REGISTRATION NUMBER: 38,304
REFERENCE/DOCKET NUMBER: A-65638/DJB/RMS
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
TELEFAX: (415) 949-8711
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 2580 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: DNA
US-09-050-863-2

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Best Local Similarity	43.28;			
Matches 276;	Conservative	0;	Mismatches 360;	Indels 3;
				Gaps 1

[illegible][illegible]

RESULT 12

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US-09-112-096-28
: Sequence 28, Application US/09112096
: Patent No. 6194152
: GENERAL INFORMATION:
:
: APPLICANT: Reiner laue
: APPLICANT: Michael H. Shapiro
: APPLICANT: Larisa Tsvaler
: TITLE OF INVENTION: Prostite Tumor Polynucleotide and
: TITLE OF INVENTION: Antigen Compositions
: FILE REFERENCE: 7636-0015-30
: CURRENT APPLICATION NUMBER: US/09/112,096
: CURRENT FILING DATE: 1998-07-09
: EARLIER APPLICATION NUMBER: 60/056,110
: EARLIER FILING DATE: 1997-08-20
: NUMBER OF SEQ ID NOS: 29
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 28
: LENGTH: 3848
: TYPE: DNA
: ORGANISM: Homo sapiens
US-09-112-096-28

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Best Local Similarity	58.0%	Pred. No.	0.031	
Matches 83, Conservative	0	Mismatches	60	Indels 0
				Gaps 0

[illegible]

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: October 4, 2001, 06:06:50 ; Search time 3270.71 Seconds
(Without alignments)
11676.325 Million cell updates/sec

Title: US-09-445-614-1

Perfect score: 2469
Sequence: 1 cacgagcgccgacgcgcagctc.....gctgctctcgggtccagct 2469

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1344157 seqs, 7733874588 residues

Total number of hits satisfying chosen parameters: 2688314

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-Processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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5	2397.8	97.1	2507	88	AF103906 Homo sapi
6	2379.4	96.4	2397	89	AF129112 Homo sapi
7	2347.8	95.1	2351	9	AX019706 Sequence
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Db 1107 GCATGCCCTAGTATGATGATCTCGGACCACTAGCTGAGAAATTTGATGCTGACACCAT 1186
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Db 1407 TGAGGGAAGACTCGAGTCTGAGATCAATGCTTTCATTTGCAAGAGCCGCAACGACACGC 1466
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RESULT 2
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DEFINITION Sequence 1 from Patent WO9946377.
ACCESSION AX017826
VERSION AX017826.1 GI:10042430
KEYWORDS
SOURCE
ORGANISM human.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 (bases 1 to 2783)
AUTHORS Renard, S. and Partlisset, M.
TITLE A human vanilloid receptor-like cation channel
JOURNAL Patent: WO 9946377-A I 16-SEP-1999;
SANOFI SYNTHELABO (FR); RENARD STEPHANE (FR); PARTISETI MICHEL (FR)
FEATURES
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BASE COUNT 578 a 824 c 796 g 585 t
ORIGIN

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Query Match 99.08; Score 2444.6; DB 9; Length 2783;
Best Local Similarity 99.78; Pired. No. 0;
Matches 2460; Conservative 0; Mismatches 4; Indels 3; Gaps 1;

QY 3 cgaagccagacgacgttgaggaagaaagagacccttgacatctcatctgacaaagg 62
DB 267 CAACACCGACGCGACGTGGAGAGAAACAGACCTTGACATCTCCATCTGCAAGG 326
QY 63 tctgtgtgacgacgacgacctctctccttagatgacctcaacctcagctctcagt 122
DB 327 TCTGTGCTGACGACGACGCTCTCTCTAGATGACCTCAACCTCCAGCTCTCAGT 386
QY 123 tttaaggttgagacatataatgagagcaagaatgctctgtgagcgagcaagaaa 182
DB 387 TTTCAGGTGAGACATTAATAGAGGCAAGAGATGCTGTAGGCGGACAGAGAAA 446
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DB 447 GCTGGATTTTGGAGGCGGCTGCTCCCATGGAGTCACTTCCAGGGCGAGACGGA 506
QY 243 attcgccctcagataagatcaacctcaactcaacgaaagagagtgccagtcacc 302
DB 507 ATTCGCCCTTCAGTAAGAGTCAACCTCACTACCGAAGGAAAGAGTCCAGTACGC 566
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QY 363 ggaatctgtgacttccagagatcctgtgacaaagacaggaagttaacctacagac 422
DB 627 GGAATCTGGCTGGACTTCCAGATGACCTGACCAAGACCAAGACCAAGTACTCCAC 686
QY 423 atcaacagagagctcccaagtgaaagctgtcgtatgaaagctgtgacacttaaga 482
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RESULT 5
AF103906 2507 bp mRNA
LOCUS AF103906 2507 bp mRNA
DEFINITION Homo sapiens vanilloid receptor-like protein (VRL) mRNA, complete cds.
ACCESSION AF103906
VERSION AF103906.1 GI:5305597
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE 1 (bases 1 to 2507)
AUTHORS Garcia,R.L., Delmas,P., Cesare,P., England,S., Liapl,A. and Wood,J.N.
TITLE Cloning and functional expression of VRL, a vanilloid receptor-like gene
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 2507)
AUTHORS Garcia,R.L. and Wood,J.N.
TITLE Direct Submission
JOURNAL Submitted (02-NOV-1998) Department of Biology, University College London, Gower St., London WC1E 6BT, United Kingdom
FEATURES Location/Qualifiers
source 1..2507

BASE COUNT	517 a	738 c	717 g	532 t	3 others
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Query Match	97.1%	Score 2397.8	DB 88	Length 2507
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AUTHORS Duckworth D M, Davis J B, and Hayes P D.
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REMARK
COMMENT

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Caterina, M.J., Rosen, T.A., Tomlinaga, M., Brake, A.J. and Julius, D.
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BASE COUNT 597 a 780 c 728 g 613 t
ORIGIN

Query Match 61.7%; Score 1522.4; DB 94; Length 2718;
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AUTHORS
Ishibashi, K.
TITLE
Molecular cloning of a stretch activated channel from rat kidney
JOURNAL
Published Only in Database (1999) In press
REFERENCE
2 (bases 1 to 2713)
AUTHORS
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Submitted (24-JUN-1999) to the DDBJ/EMBL/GenBank databases. Kenichi
Ishibashi, Jichi Medical School, Pharmacology; Minami-Kawachi,
Kawachi, Tochigi 329-0498, Japan (E-mail: kishiba@jichi.ac.jp,
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RESULT 13

AB022332

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AB022332 2890 bp mRNA ROD 12-01-APR-2000
 Rattus norvegicus mRNA for ion channel from kidney, complete cds.

AB022332.1 GI:7415516
 ion channel.
 Rattus norvegicus
 Rattus norvegicus male kidney cDNA to mRNA.
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 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
 Rattus

1 (sites)
 Suzukl.M.
 Ion channel
 Unpublished (1999)
 2 (bases 1 to 2890)
 Suzukl.M.
 Direct Submission
 Submitted (12-JAN-1999) to the DDBJ/EMBL/GenBank databases. Makoto
 Suzukl, Ichih Medical School, Pharmacology, 331-1, Yakushiji,
 Minamikawachi, Tochi 329-0498, Japan (E-mail: macsuz@ichi.ac.jp,

COMMENT Tel: 81-28-558-7326, Fax: 81-28-544-5541
Sequence updated (27-Apr-1999).
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ORIGIN

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 VERSION AX019708.1 GI:10043550
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 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 885)
 AUTHORS Duckworth, D.M., Davis, J.B. and Hayes, P.D.
 TITLE Human vanilloid receptor homologues
 JOURNAL Patent: WO 9937765-A 3 29-JUL-1999;
 SMITHKLINE BEECHAM PLC (GB)
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3	2359	96.3	2380	20	AAAB7492	Human vanilloid re
4	2249	91.1	2351	20	AAZ07114	Human vanilloid re
5	2168	87.8	2783	20	AAZ22829	Human vanilloid re
6	2057	83.3	2348	20	AAZ07116	Human vanilloid re
7	1340	54.3	2765	21	AAAI4874	DNA encoding a var
8	1014	41.1	2779	19	AAV59691	Human secreted pro
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11	541	21.9	884	20	AAAI9741	Human VRRP-1 (VR2)

12	541	21.9	885	20	AAZ07115	Human vanilloid re
13	508	20.6	2860	19	AAV58017	Human secreted prot
14	472	19.1	876	19	AAV55808	Human secreted prot
15	329	13.3	350	20	AAAX8749	Human secreted prot
16	339	13.3	350	20	AAAX19739	Human vanilloid re
17	300	12.2	764	20	AAAX87500	Human VRRP-1 (VR2)
18	300	12.2	764	20	AAAX19740	Human vanilloid re
19	285	11.5	403	21	AAZ68276	Human VRRP-1 (VR2)
20	126	5.1	650	20	AAAX87481	Human colon cancer
21	126	5.1	650	20	AAAX19733	Human vanilloid re
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23	117	4.7	768	20	AAAX19732	Human vanilloid re
24	68	2.8	273	20	AAAX87479	Human VRRP-1 capse
25	68	2.8	273	20	AAAX19731	Human vanilloid re
26	44	1.8	1794	21	AAAX30236	Human VRRP-1 capse
27	44	1.8	2736	20	AAAX87478	Rat partial VR-2 c
28	44	1.8	2736	20	AAAX19730	Rat vanilloid rece
29	27	1.1	49	20	AAAX87484	Rat VRRP-1 (VR2) c
30	27	1.1	49	20	AAAX19738	Vanilloid receptor
31	27	1.1	2520	21	AAAC66463	VRRP-1 capsaicin r
32	27	1.1	2544	20	AAAX87491	Human vanilloid re
33	27	1.1	3500	20	AAZ10065	Human capsaicin re
34	27	1.1	3909	21	AAA30253	CDNA encoding a hu
35	27	1.1	4365	21	AAA29172	Human VR-1 coding
36	27	1.1	4803	20	AAZ10062	Human vanilloid re
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38	27	1.1	4824	21	AAAC6464	CDNA encoding a pa
39	22	0.9	4012	22	AAAX14891	Human vanilloid re
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44	21	0.9	21	21	AAAX14876	PCR primer J2 for
45	21	0.9	21	21	AAAX14877	PCR primer J3 for

ALIGNMENTS

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AC	AAC60297;
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DT	14-FEB-2001 (first entry)
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DE	Human vanilloid receptor like receptor DNA.
XX	
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KW	mechanical injury; lymphoid tissue; human; ds.
XX	
OS	Homo sapiens.
XX	
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PF	02-DEC-1999; 99GB-0028566.
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PR	08-DEC-1998; 98GB-0027016.
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PA	(MERI) MERCK SHARP & DOHME LTD.
XX	
PI	Bonnert TP;
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DR	WPI; 2001-064250/08.
XX	
DR	P-PSDB; AAB35622.
XX	
PT	New polynucleotide encoding human vanilloid receptor-like receptor for
PT	diagnosing and treating pain, infections, allergies, and cancers
XX	
OS	Claim 2; Fig 1; 36pp; English.

XX The present invention relates to the human vanilloid receptor-like
CC receptor. This receptor may be used for diagnosing or treating
CC conditions associated with altered vanilloid receptor-like (VR-L)
CC receptor expression. It may also be used to treat abnormal conditions
CC associated with pain. Conditions or diseases that can be diagnosed or
CC treated include viral, bacterial and fungal infections, allergic
CC responses, mechanical injury associated with trauma, hereditary
CC diseases, lymphoma or carcinoma, or other conditions which activate
CC the genes of the lymphoid tissues.

Sequence 2469 BP; 510 A; 724 C; 710 G; 525 T; 0 other;

Query Match	100.0%	Score 2469;	DB 22;	length 2469;
Best Local Similarity	100.0%	Pred. No. 0;		
Matches 2469; Conservative	0;	Mismatches	0;	Gaps 0;

[illegible]

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Db	1561	tctctggcatacgaatggtatacctctgcagccctgctgtgtgtctgcgctgagctgctggctgctg	1620
QY	1621	aacctggtttactatacaacgttggtcttcacagacacaagagatactacaagtgtcaatgatacga	1680
Db	1621	aacctggtttactatacaacgttggtcttcacagacacaagagatactacaagtgtcaatgatacga	1680
QY	1681	aagatcatactctggcggaacactgctgcgctcttctcttgatacttgatctctccttctgc	1740
Db	1681	aagatcatactctggcggaacactgctgcgctcttctcttgatacttgatctctccttctgc	1740
QY	1741	ttcgcgtgtaaacctgtgtgaacctcgaaacagagaggtcttggtgcgccgaaagctctcaacgc	1800
Db	1741	ttcgcgtgtaaacctgtgtgaacctcgaaacagagaggtcttggtgcgccgaaagctctcaacgc	1800
QY	1801	cccacatcccaagatgcagatgcagcccaatggaggggaacagaaagaaagagaggaacggggcc	1860
Db	1801	cccacatcccaagatgcagatgcagcccaatggaggggaacagaaagaaagagaggaacggggcc	1860
QY	1861	caatacaagggtatactctgtgaagacctctcttgagactcttccaataatccatcggatgggc	1920
Db	1861	caatacaagggtatactctgtgaagacctctcttgagactcttccaataatccatcggatgggc	1920

Oy	1921	gacgtcgccttcgaaggagcagcgccacttccggagatagtgtcgtcgtcgtcgtcgc	1980
Db	1921	gagctgaccttcgaaggagcagcgccacttccggagatagtgtcgtcgtcgtcgtcgc	1980
Oy	1981	tacgtctcgtccaccacatactccgtcgtccaatatgtcatctgccctccatgaggagaac	2040
Db	1981	tacgtgctgtccaccacatactccgtcgtccaatatgtcatctgccctccatgaggagaac	2040
Oy	2041	gtcaaacagtgtcgcaccactgacaagcttgagagatcttgaaagctgcaaagacattctgtc	2100
Db	2041	gtcaaacagtgtcgcaccactgacaagcttgagagatcttgaaagctgcaaagacattctgtc	2100
Oy	2101	cctggagatctggaagatctgatctgtgtctgcagaagaagacagcggagagctgtatgtctg	2160
Db	2101	cctggagatctggaagatctgatctgtgtctgcagaagaagacagcggagagctgtatgtctg	2160
Oy	2161	accgtttggacaactaagccaatgtgcaagcccggatgagcgcgtgtcttaagggtctgaaagag	2220
Db	2161	accgtttggacaactaagccaatgtgcaagcccggatgagcgcgtgtcttaagggtctgaaagag	2220
Oy	2221	gtcaactcgtggtcttaactgtaggagcagacgctgtcctaagctgtgtctaggaacccgctcaggagca	2280
Db	2221	gtgaactcgtggtcttaactgtaggagcagacgctgtcctaagctgtgtctaggaacccgctcaggagca	2280
Oy	2281	ggtgtccctctcgaaactctcgaagaacccctgtctctgtgcttccccctcccaaggagagatgaagat	2340
Db	2281	ggtgtccctctcgaaactctcgaagaacccctgtctctgtgcttccccctcccaaggagatgaagat	2340
Oy	2341	ggtgtcctctcgaaagaaaactatgtgtcccggtccagctctctccatgtccaactgtatgtcccaaga	2400
Db	2341	ggtgtcctctcgaaagaaaactatgtgtcccggtccagctctctccatgtccaactgtatgtcccaaga	2400
Oy	2401	tgcacgacgagagcgcacagagacagagagagagatcttccaaacacatctgtctgtctcttg	2460
Db	2401	tgcacgacgagagcgcacagagacagagagagagatcttccaaacacatctgtctgtctcttg	2460
Oy	2461	ggtccccaagt 2469 	
Db	2461	ggtccccaagt 2469 	
RESULT 2			
ID	AAA30254		
AC	AAA30254 standard; cDNA; 2809 BP.		
XX	AAA30254;		
DT	05-SEP-2000 (first entry)		
DE	Human VR-2 coding sequence.		
XX			
KM	VR-2; human; vanilloid receptor; nociceptor; pain signalling; hyperalgesia; musculoskeletal disorder; neuropathic pain; chromosome 1/p11-12; gene therapy; ss.		
OS	Homo sapiens.		
XX			
FH	Key	Location/Qualifiers	
FT	CDS	361..2655	
FT		/tag= a	
FT		/product= "VR-2"	
XX		/note= "This region is specifically claimed"	
PN	WO200029577-A1.		
XX			
PD	25-MAY-2000.		
PF	12-NOV-1999;	99WO-US26701.	
XX			
PR	13-NOV-1998;	98US-0108322.	
PR	26-DEC-1998;	98US-0114078.	
PR	26-FEB-1999;	99US-0258633.	
PR	19-OCT-1999;	99US-0421134.	

XX (MILL-) MILLENNIUM PHARM INC.
PA
XX
PI Curtis RAJ;
XX
DR WPI: 2000-387790/73.
P-PsDB; AAY97358.
XX
PT New capsactin/vanilloid receptor polynucleotides and polypeptides, used
PS to modulate pain signalling mechanisms -
XX

Claim 1; Fig 2; 183pp; English.

The present sequence is the coding sequence for human capsacin/vanilloid receptor VR-2, which is involved in pain signalling. The sequence was isolated by searching a heart library for genes encoding novel receptors of the capsacin/vanilloid family, and has been shown to be located at chromosome 17p11-12. This region has been associated with myasthenia gravis, Smith-Wagenis syndrome, CORDS, cone-rod dystrophy, choroidal dystrophy, central areolar and retinal cone dystrophy, and it is possible that the protein may be used to treat or diagnose these disorders. In addition, the gene, protein and its antibodies can be used to diagnose and treat hyperalgesia, inflammation, infection, ischemia, joint pain, tooth pain, headaches, pain associated with surgery or neuropathic pain, possibly via the use of gene therapy.

SQ Sequence 2809 BP; 601 A; 825 C; 798 G; 585 T; 0 other;

Query Match	99.7%	Score 2462	DB 21	Length 2809
Best Local Similarity	100.0%	Pred. No. 0		
Matches 2462; Conservative	0	Mismatches	0	Gaps 0

QY	8	cogaaagcgcacgctctgtagagaaagacagagcccttgaacatctccatctcgacagagctccg	67
Db	272	ccgaagccgcacgctctgtagagaaagacagagcccttgaacatctccatctcgacagagctccg	331
QY	68	gctgtagaccgagacagagctctctctctccaaagagactccacccctccagagctctccatttca	127
Db	332	gctgtagaccgagacagagctctctctctccaaagagactccacccctccagagctctccatttca	391
QY	128	ggctgtagagacattgaatgtagagcgcaagaaagaatggctctgagagcgagacagagaaagcttg	187
Db	392	ggctgtagagacattgaatgtagagcgcaagaaagaatggctctgtagagcgagacagagaaagcttg	451
QY	188	attttggagagagcgcgctctgctctcccatctgtagcttcaacgcttccagagcgagagaccgaattcg	247
Db	452	attttggagagagcgcgctctgctctcccatctgtagcttcaacgagcttccagagcgagagaccgaattcg	511
QY	248	cccccacagataagatcacaacctccaaactacccgaaagagggagaaagctgacagctcaagccgagatc	307
Db	512	cccccacagataagatcacaacctccaaactacccgaaagagggagaaagctgacagctcaagccgagatc	571
QY	308	caaaacggaatttgacccgagagatcgagctctcaaatgctgctccccgggggtgtccccgagagatc	367
Db	572	caaaacggaatttgacccgagagatcgagctctcaaatgctgctccccgggggtgtccccgagagatc	631
QY	368	tggctgagagcttcccgagagatcaacctctgtagcaagagacaaagatcaactcaacgagatcggaaataca	427
Db	632	tggctgagagcttcccgagagatcaacctctgtagcaagagacaaagatcaactcaacgagatcggaaataca	691
QY	428	cagaagagctcccaacagtgtaagaacgtgacctgataagagagcgctctgctgtaaaccttaagaaagag	487
Db	692	cagaagagctcccaacagtgtaagaacgtgacctgataagagagcgctctgctgtaaaccttaagaaagag	751
QY	488	tcaatgctctgcatctctgcacactgctgcaagatcgagacaaagagagactctgccaatccctcaagccc	547
Db	752	tcaatgctctgcatctctgcacactgctgcaagatcgagacaaagagagactctgccaatccctcaagccc	811
QY	548	tggtagaaatggcccagattgacaaatgaaactcttaacccgagagcccaagagcgctctgcaaatcgcca	607
Db	812	tggtagaaatggcccagattgacaaatgaaactcttaacccgagagcccaagagcgctctgcaaatcgcca	871

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FT CDS 19..2316
 FT /tag= a
 XX MO937675-A1.
 XX 29-JUL-1999.
 XX
 XX 22-JAN-1999; 99WO-US01418.
 XX
 XX 22-JAN-1998; 98US-0072151.
 XX
 PA (REGC) UNIV CALIFORNIA.
 XX
 PI Brake AJ, Caterina M, Julius DJ;
 XX
 XX WPI: 1999-469113/39.
 DR P-PSDB; AAY06559.
 XX
 PT New isolated capsaicin receptor polypeptide and related nucleic acid
 PT - useful for detecting vanilloid compounds, identifying modulators,
 PT and in diagnosis or treatment of e.g. pain and inflammation
 XX
 PS Claim 8; Page 107-110; 120pp; English.
 XX
 CC This is the nucleotide sequence of cDNA coding for human vanilloid
 CC receptor-related polypeptide 1 (VRP-1 or VR2). The cDNA was
 CC isolated from a CCRF-CM cell cDNA. VRP-1 (AAY06559) is an example
 CC of a capsaicin receptor-related polypeptide of the invention. It
 CC is not activated by capsaicin or heat, but may interact with the
 CC novel capsaicin receptor VR1 (see AAY06558). The invention provides
 CC vanilloid receptor polypeptides and polynucleotides, including
 CC capsaicin receptor-related polypeptides and polynucleotides, as well
 CC as expression vectors, host cells and transgenic animals. It also
 CC provides a method of using such receptors to identify vanilloid
 CC compounds in natural products or to screen candidate compounds that
 CC modulate capsaicin receptor function for use as analgesics (vanilloid
 CC analogues, therapeutic antibodies, antisense oligonucleotides,
 CC capsaicin receptor-encoding polynucleotides for gene therapy),
 CC flavour-enhancing agents, etc. Capsaicin receptor-related
 CC polypeptides and specific antibodies can also be used for the
 CC diagnosis and treatment of human disease and pain. Polynucleotides
 CC can be used as probes to determine the structure, function, location
 CC and expression of capsaicin receptor, receptor subtypes and capsaicin
 CC receptor-related polypeptides in mammals (including humans) and to
 CC investigate associations between disease states or clinical disorders
 CC (particularly those involving acute and chronic pain or inflammation)
 CC and defects or alterations in receptor structure, expression or
 CC function.
 CC
 CC Sequence 2380 BP; 491 A; 698 C; 678 G; 513 T; 0 other;
 SQ

Query Match 94.3%; Score 2329; DB 20; Length 2380;
 Best Local Similarity 100.0%; Pred. NO. 0;
 Matches 2379; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 241 gacagagatcggtcttcaatcggtctccgggtgtcccgagatctggtgact 300
 |||||||
 QY 379 ccagagttacttgaagaagaccagcaagtaacctaccagctcggatatacagaaggctcc 438
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 Db 301 ccagagttacttgaagaagaccagcaagtaacctaccagctcggatatacagaaggctcc 360
 |||||||
 QY 439 acaggttaagacgtgtcgtatgaagctgtgtcgaacctaaagacggagtcattgtctgc 498
 |||||||
 Db 361 acaggttaagacgtgtcgtatgaagctgtgtcgaacctaaagacggagtcattgtctgc 420
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 QY 499 attctgcaactctgcagatcagacaggagctctgtgcaacctcccaacctgttaattgcc 558
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 Db 421 attctgcaactctgcagatcagacaggagctctgtgcaacctcccaacctgttaattgcc 480
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 QY 559 cagttcacagatgactatattaccagagccacagcgctctgcacatgcacattgagaagag 618
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 Db 481 cagttcacagatgactatattaccagagccacagcgctctgcacatgcacattgagaagag 540
 |||||||
 QY 619 agctgcaggtgtgtgaagctctctgtgtgagaatggtggccaatgtcatgcccggcttcg 678
 |||||||
 Db 541 agctgcaggtgtgtgaagctctctgtgtgagaatggtggccaatgtcatgcccggcttcg 600
 |||||||
 QY 679 ggcgccttctccagaaggcccaaggagacttcttatttcgtgtgactaccctctct 738
 |||||||
 Db 601 ggcgccttctccagaaggcccaaggagacttcttatttcgtgtgactaccctctct 660
 |||||||
 QY 739 ttgscgcttgacccaagcagtggtgtgtgttaagctactcctctggaagaccacacag 798
 |||||||
 Db 661 ttgscgcttgacccaagcagtggtgtgtgttaagctactcctctggaagaccacacag 720
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 QY 799 ccgcgcacccctgcagggccacagctgactcccaaggccaacacagtcctgcatgacctagt 858
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 Db 721 ccgcgcacccctgcagggccacagctgactcccaaggccaacacagtcctgcatgacctagt 780
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 |||||||
 Db 781 atctggaacactcagctcagagaaacattgcatgtgtgacagcatgtatgaggtctctc 840
 |||||||
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 Db 841 caagctggggccgcgcctctgcctacacgtgacgttgagatcgcgaacctgcagat 900
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 QY 979 ctccgcctctggaagctgtgcgccaaggagggcaagatcggatctttagcacatctgt 1038
 |||||||
 Db 901 ctccgcctctggaagctgtgcgccaaggagggcaagatcggatctttagcacatctgt 960
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 QY 1039 cagcggagtttccagagctgagccaccttcccgaaagttcacccagatgtgtctatgg 1098
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 Db 961 cagcggagtttccagagctgagccaccttcccgaaagttcacccagatgtgtctatgg 1020
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 QY 1099 cctgtccgggtgtcgtcgtatgacctgtgtctgtgacagctgtgaggaactcagtg 1158
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 Db 1141 ccccttgacaacactgcgcagcgcaaatgagatctgtcctacatcccaagttcttctaac 1200
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 QY 1279 ttctgtgttaactgtatctatcatcttcaacgcgtgtgtcctaaccatcagctaac 1338
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 Db 1201 ttctgtgttaactgtatctatcatcttcaacgcgtgtgtcctaaccatcagctaac 1260
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 Db 1261 ctgagaagacgagcgcccccacactgaagaagcggaagttgaaactctcagctgtcag 1320
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[illegible]

ID	AAZ07114 standard; cDNA: 2351 BP
XX	
AC	AAZ07114;
XX	
DT	08-OCT-1999 (first entry)
DE	
XX	
XX	Human vanilloid receptor homologue.VANILREBP2 encoding cDNA.
KM	Human; vanilloid receptor homologue; VANILREBP2; polymorphic variant;
KW	PVP-1; therapy; diagnosis; chronic pain; neuropathic; postoperative;
KW	rheumatoid arthritis; neuralgia; algesia; nerve injury; ischemia;
XX	neurodegeneration; stroke; incontinence; inflammatory disorder; ss.
OS	Homo sapiens.
XX	
FH	Key
FT	Location/Qualifiers
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PN	WO937765-A1.
XX	
PD	29-JUL-1999.
XX	
PF	25-JAN-1999; 99WO-EP00420.
XX	
PR	20-JAN-1999; 99GB-0001209.
PR	27-JAN-1998; 98EP-0300549.
PR	26-OCT-1998; 98GB-0023421.
XX	
PA	(SMIK) SMITHKLINE BEECHAM PLC.
PI	Davis JB, Duckworth DM, Hayes PD;
DR	WPI: 1999-479049/40.
DR	P-PsDB: AAY29469.
XX	
PT	New human vanilloid receptor homologues (VANILREBP2)
PS	Claim 9; Page 29-30; 47pp; English.
XX	
CC	The present sequence encodes a human vanilloid receptor homologue,
CC	designated VANILREBP. VANILREBP2 can be used to diagnose disease or
CC	susceptibility to disease related to expression or activity of
CC	VANILREBP2 polypeptides. VANILREBP2 may be used to treat diseases
CC	including pain, (for example chronic, neuropathic, postoperative,
CC	rheumatoid arthritis), neuralgia, algesia, nerve injury, ischaemia,
CC	neurodegeneration, stroke, incontinence, and inflammatory disorders.
XX	
SQ	Sequence 2351 BP; 486 A; 684 C; 676 G; 505 T; 0 other:

Query Match	91.1%; Score 2249; DB 20; Length 2351;
Best Local Similarity	99.9%; Pred. No. 0;
Matches 2349; Conservative	0; Mismatches 2; Indels 0; Gaps 0;

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OY	153 agaaatgagctctgagggcgagacaaggaaagcttgatttggagcgggcctcccat	212
Db	61 agaagatgagctctgagggcgagacaaggaaagcttgatttggagcgggcctcccat	120
OY	213 ggaatcacagttccaggcgagacggagaatttcgccctcagataaagtaactcaa	272
Db	121 ggaatcacagttccaggcgagacggagaatttcgccctcagataaagtaactcaa	180
OY	273 ctaccgaaagggaacaggtgcacagtcacacggatcccaacgattgacgagatcgct	332
Db	181 ctaccgaaagggaacaggtgcacagtcacacggatcccaacgattgacgagatcgct	240

QY	333	cttcaatctgctgtctcccggtgtgtctcccgagatctctgctcgaagtacctcgtag	392
Db	241	cttcaatctgctgtctcccggtgtgtctcccgagatctctgctcgaagtacctcgtag	300
QY	393	caagacacgaagtaccttcacccgaactctggaataacagagaggtccacaaagttaagacgtg	452
Db	301	caagacacgaagtaccttcacccgaactctggaataacagagaggtccacaaagttaagacgtg	360
QY	453	ccctgataagagctgtctgtcaaaccttcataaagagagagctcaatctctgtcaactgtct	512
Db	361	ccctgataagagctgtctgtcaaaccttcataaagagagaggtcaatctctgtcaactgtct	420
QY	513	gcagatctgacagagacctctgtgcaatctcctcagccctctgtgtaaatgcccagtgtcacagtga	572
Db	421	gcagatctgacagagacctctgtgcaatctcctcagccctctgtgtaaatgcccagtgtga	480
QY	573	catattacccagagccacagacgtctctgcaacatcgtccatttgaaagaagaggtctctgaagctgt	632
Db	481	catattacccagagccacagacgtctctgcaacatcgtccatttgaaagaagaggtctctgaagctgt	540
QY	633	gaagctctctgtctggaagatctgggcgaatgtgtacagccccggccctgtgcgcgcctcttcca	692
Db	541	gaagctctctgtctggaagatctgggcgaatgtgtacagccccggccctgtgcgcgcctcttcca	600
QY	693	gaagggccaaagagacgtcttattatcttcgtgtagactaacccctctctctgtgcgcgtgtgac	752
Db	601	gaagggccaaagagacgtcttattatcttcgtgtagactaacccctctctctgtgcgcgtgtgac	660
QY	753	caagagagtggaatgtgtgaagcttaccctccctggagaaacccacacacccgccaagctgtga	812
Db	661	caagagagtggaatgtgtgaagcttaccctccctggagaaacccacacacccgccaagctgtga	720
QY	813	ggccacctgacccccaagggcaacacagctccctgtcacgtgtgatatctctgcgaacaactc	872
Db	721	ggccacacgtgacccccaagggcaacacagctccctgtcacgtgtgatatctctgcgaacaactc	780
QY	873	agctgtagaacatctgcactgtgtgacacagcatgtatgtatggtctctccaaagctgtgggcccg	932
Db	781	agctgtagaacatctgcactgtgtgacacagcatgtatgtatggtctctccaaagctgtgggcccg	840
QY	933	ccctctggccctacccgttgagacgtcttgagacatccgcacacctgtgcagatctcacgcctctgaa	992
Db	841	ccctctggccctacccgttgagacgtcttgagacatccgcacacctgtgcagatctcacgcctctgaa	900
QY	993	gctgtgcgcgcgaagagggcaagatcagatattctcagagacacatccctgcagccggagatttc	1052
Db	901	gctgtgcgcgcgaagagggcaagatcagatattctcagagacacatccctgcagccggagatttc	960
QY	1053	aggacctgagacacctctcccgaaagtctacacgagctgtgctatgtggtcgtgtccgggtgtc	1112
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QY	1173	cttcatattgcagaagcccgcgacacgcgaacacccgaatgtgtgtcttggaagccctctgaanaaact	1232
Db	1081	cttcatattgcagaagcccgcgacacgcgaacacccgaatgtgtgtcttggaagccctctgaanaaact	1140
QY	1233	gtctgcagagcgaaatgtggtatctgtctatccccaagtctctctcttaaaactctctgtgtaact	1292
Db	1141	gtctgcagagcgaaatgtggtatctgtctatccccaagtctctctcttaaaactctctgtgtaact	1200
QY	1293	gattataatgttatcttctacacgcgtgtctcctacatcagcctacacctgaagaagcagc	1352
Db	1201	gattataatgttatcttctacacgcgtgtctcctacatcagcctacacctgaagaagcagc	1260
QY	1353	cgccccctacactgaaagcggaggtcttgaaacccatgtctgtcgtcgaagggccacatcccttat	1412
Db	1261	cgccccctacactgaaagcggaggtcttgaaacccatgtctgtcgtcgaagggccacatcccttat	1320
QY	1413	ctgtgtcaggggagatcbacacctctctgtgtgggcagactgtgtgtaactctctgtgcgcgcacgt	1472

Dh	1321	cctgcaagagggagacatcaaccctcccgctgagccagccctgctgtaactcttcgctgagccacagt	1381
Qy	1473	gttcatactctgaaactctgtttcatagaaagacatactctgaaatccctctctctgtcttcaagccct	1533
Dh	1381	gttcatactgatactctgttcatatagaaagataactcttgaaatccctctctctgtcttcaagccct	1441
Qy	1533	gtctcaagatgctgtctccaaagctgctgtgtttcttcctgagccacacgagctgtatactctgacctgct	1593
Dh	1441	gtctcaacagatgctgtctccaaagctgctgtgtgtttcttcctgagccacacgagctgtatactctgacctgct	1501
Qy	1593	tctgtctgagcgcgtgctggggtctggtactgtacttactatacaagctgtgcttccagca	1653
Dh	1501	tgtgtctcgagcgcgtgctggggtctggtactgtacttactatacaagctgtgcttccagca	1561
Qy	1653	caacagagcatctcaagctgtctatgatactccaaagaagctatccctcgaggaacctgtgtgagctctct	1713
Dh	1561	caacagagcatctcaagctgtctatgatactccaaagaagctatccctcgaggaacctgtgtgagctctct	1621
Qy	1713	tctgatactaatgactctccctcttcctgagctctgctgtatagccctctgctgagccctgagccagag	1773
Dh	1621	tctgatactaatgactctccctcttcctgagctctgctgtatagccctctgctgagccctgagccagag	1681
Qy	1773	ggctctggagcccccagagctctcttaagagccccaatgccaacagaaatcagctgcaagcccatgga	1833
Dh	1681	ggctctggagcccccagagctctcttaagagccccaatgccaacagaaatcagctgcaagcccatgga	1741
Qy	1833	ggagacaagagagacagagggcaaacaggggagccaaagttaaaggggtatccctgaggaagccctcttga	1893
Dh	1741	ggagacaagagagacagagggcaaacaggggagccaaagttaaaggggtatccctgaggaagccctcttga	1801
Qy	1893	gctcttcaaatcaacatccgacatgagcattgagcagagctgagcccttcacagagacatgcaacttcag	1953
Dh	1801	gctcttcaaatcaacatccgacatgagcattgagcagagctgagcccttcacagagacatgcaacttcag	1861
Qy	1953	cgagcaatgctgtgctgtctgctgcagcagcgtcagccctgagcttactataatccctgctgtctaa	2013
Dh	1861	cgagcaatgctgtgctgtctgctgcagcagcgtcagccctgagcttactataatccctgctgtctaa	1921
Qy	2013	catgctatactgacccctcatctgaagcagaaacagctcaacaaagatgctgcacacatgaaacgtctgaagcat	2073
Dh	1921	catgctatactgacccctcatctgaagcagaaacagctcaacaaagatgctgcacacatgaaacgtctgaagcat	2033
Qy	2073	ctgagaaagctgcaagaagaagccatctctgtctcctgagagatgagaaatgagctatgtgctgagag	2133
Dh	2033	ctgagaaagctgcaagaagaagccatctctgtctcctgagagatgagaaatgagctatgtgctgagag	2041
Qy	2133	gaaagaaagagagggagcagctgtgtaagctcgaacccgttggcacttaagccaaagatgagagcccgga	2193
Dh	2041	gaaagaaagagagggagcagctgtgtaagctcgaacccgttggcacttaagccaaagatgagagcccgga	2101
Qy	2193	tgaagcagctgagctctcaagggctgagagagagctgaaacctgagcttcaatctgagaaacaaagctctgc	2253
Dh	2101	tgaagcagctgagctctcaagggctgagagagagctgaaacctgagcttcaatctgagaaacaaagctctgc	2161
Qy	2253	tacagctgtgtgagagagcccgctcaaggggacagctgtctctccctcgaactctctgagaaacccctgtct	2313
Dh	2161	tacagctgtgtgagagagcccgctcaaggggacagctgtctctccctcgaactctctgagaaacccctgtct	2221
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Dh	2221	ggctctcccccctccaaagagaaatgagaaatgagctgtgctctctgagagaaacatagtgtgcccgtcca	2281
Qy	2373	gctctctcaatccaaactgagcagcagaaatgagccaaagaaagcagaagagagcagaagagagaa	2433
Dh	2281	gctctctcaatccaaactgagcagcagaaatgagccaaagaaagcagaagagagcagaagagagaa	2341
Qy	2433	tctttccaacc 2443	
Dh	2341	tctttccaacc 2351	

ID	AAZ22829	standard; cDNA; 2783 BP.
AC	AAZ22829;	
DT	06-DEC-1999	(first entry)
DE	Human vanilloid receptor-like cation channel (hVRCC) cDNA.	
KW	Vanilloid; capsaicin; neuron; selective; calcium; cation; receptor; pain; inflammation; brain disease; cancer; autoimmune disorder; ds.	
OS	Homo sapiens.	
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XX	FT	/*tag- e
XX	FT	replace (750, G)
XX	FT	/*tag- f
XX	FT	replace (787, C)
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XX	FT	replace (1612, CAGG)
XX	FT	/*tag- h
XX	FT	2653..2783
XX	FT	/*tag- l
XX	MO3946377-A2.	
XX	16-SEP-1999.	
XX	10-MAR-1999;	99WC-EP01550.
XX	11-MAR-1998;	98EP-0400565.
XX	(SNFI) SANOFI-SYNTHELABO.	
XX	Partisettl M, Renard S;	
XX	WPI; 1999-571722/48.	
XX	P-PSDB; AAY42308.	
XX	New receptor-like channel polypeptide and polynucleotide useful for prevention and treatment of cancer, autoimmune disease, brain disease and ulcers	
XX	Claim 5; Page 14; 50pp; English.	
XX	This sequence represents a human vanilloid receptor-like cation channel (hVRCC) cDNA. This channel is activated by vanilloids such as capsaicin and resiniferatoxin, and is expressed in a variety of tissues, particularly in nervous tissue such as the amygdala, substantia nigra, thalamus, dorsal root ganglia and spinal cord. Vanilloids are natural compounds which are known to trigger cation permeability in the peripheral neurons involved in transmission of noxious stimuli (e.g., mechanical, chemical or thermal). A recently discovered rat vanilloid-gated cation channel, which is highly expressed in dorsal root ganglia, has six putative transmembrane domains, giving it significant structural homology with "store-operated" calcium channels, and is highly selective for calcium ions. hVRCC and nucleotides encoding it can be used in prevention, diagnosis or therapy of disorders that may be associated with an excess or deficiency of hVRCC. Disorders detected or treated using hVRCC proteins, nucleotides or antagonists include chronic inflammation, acute and chronic pain, brain diseases, abnormal proliferation and cancer, ulcers, autoimmune diseases, control of visceral effect of endogenous neurotransmitters and hormones, and to inhibit graft rejection by promoting immunosuppression. Nucleotide sequences encoding hVRCC are also useful for chromosome localisation.	

XX	Sequence	2783 BP; 578 A; 824 C; 796 G; 585 T; 0 other;
SQL	Query Match Best Local Similarity Matches 2458; Conservative	87.8%; Score 2168; DB 20; Length 2783; 99.8%; Pred. No. 0; 0; Mismatches 1; Indels 3; Gaps
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DB	272 ccgagccgcagcagctcggaggaagacaggaaccccttgacaatctccatctcagcaagagctctg	331
QY	68 gcttgagccgagagcagcctctctctctctctagatgacacccctccagctctccagatttca	127
DB	332 gcttgagccgagagcagcctctctctctctctagatgacacccctccagctctccagatttca	391
QY	128 ggttggaagacattgagtgaggagccaaagaaatggctctggaggaggagccaaagaaagctgg	187
DB	332 ggttggaagacattgagtgaggagccaaagaaatggctctggaggaggagccaaagaaagctgg	451
QY	188 attctggagagcggcctctgcccctcccatctggagagcacaagcttccagggccgagagacatcg	247
DB	452 attctggagagcggcctctgcccctcccatctggagagcacaagcttccagggccgagagacatcg	511
QY	248 cccctcagataagatgtcaacctcaactcaaccgaaagaggaacaggtgtccagtcacgcggatc	307
DB	512 cccctcagataagatgtcaacctcaactcaaccgaaagaggaacaggtgtccagtcacgcggatc	571
QY	308 caaacccgatttgacccggagatccggctctctcaatgtcgctctcccggggtgtcccccggagtc	367
DB	572 caaacccgatttgacccggagatccggctctctcaatgtcgctctcccggggtgtctcccccggagtc	631
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QY	428 cagaagagctccacaagagtgaagacgtgtccctgataggaagctgtgtcgtgaaccttaagagacggag	487
DB	692 cagaagagctccacaagagtgaagacgtgtccctgataggaagctgtgtcgtgaaccttaagagacggag	751
QY	488 tcaatgctctgtcatctctgccaactctgctcagatctgcaacagagacctctgccaatctctcagcccc	547
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Db 2729 gt 2730

RESULT 6
AAZ07116
ID AAZ07116 standard; cDNA; 2348 BP.
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AC AAZ07116;
XX
DT 08-OCT-1999 (first entry)
XX
DE Human vanilloid receptor homologue VANILREP2 polymorphic variant PVP-1.
XX
KW Human; vanilloid receptor homologue; VANILREP2; polymorphic variant;
KW PVP-1; therapy; diagnosis; chronic pain; neuropathic; postoperative;
KW rheumatoid arthritis; neuralgia; algosia; nerve injury; ischemia;
KW neurodegeneration; stroke; incontinence; inflammatory disorder; ss.
XX
OS Homo sapiens.
XX
FH Key
FH CDS
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FT /note- "vanilloid receptor homologue"
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PD 29-JUL-1999.
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PF 25-JAN-1999; 99MO-EP00420.
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PR 20-JAN-1999; 99GB-0001209.
PR 27-JAN-1998; 98EP-0300549.
PR 26-OCT-1998; 98GB-0023421.
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PA (SMK ) SMITHKLINE BEECHAM PLC.
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PI Davis JB, Duckworth DM, Hayes PD;
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DR WPI: 1999-479049/40.
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DR P-PDB; AAT29471.
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PT New human vanilloid receptor homologues (VANILREP2)
XX

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RESULT	7
ID	AAA14874 standard; DNA; 2765 BP.
AC	AAA14874;
DT	08-AUG-2000 (first entry)
DE	DNA encoding a vanilloid receptor-like (VR-L) protein.
KW	Calciton channel protein; vanilloid receptor-like 1 protein; VR-L;
KW	noxious heat; pain; inflammation; tissue damage; nociception;
KW	gene therapy; sensory neuron; immune system; analgesic; immunomodulatory;
XX	neuromodulatory; ss.
OS	Homo sapiens.
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PN	WO200022121-A2.
XX	20-APR-2000.
PD	XX
PF	08-OCT-1999; 99WO-GB03348.
PR	09-OCT-1998; 98GB-0022124.
PA	(UNLO) UNIV COLLEGE LONDON.
XX	XX
PI	Garcia R, Wood JN, England S;
DR	WPI; 2000-317978/27.
DR	P-PSDB; AAY84834.

xx Novel non-selective cation channel protein and nucleotides useful as
 pr screening agents and in gene therapy of disorders associated with
 pr sensory neurons and leucocytes such as pain, autoimmune disorders and
 pr leukemias

Claim 5; Fig 3A; 55pp; English.

The present sequence encodes a non-selective cation channel protein, designated vanilloid receptor-like 1 (VR-1). The protein is obtained from human T lymphocytes. The VR-1 protein is activated by noxious heat, and is not capsaicin sensitive. VR-1 is expressed in sensory neurons, and is likely to play a role in mediating the pain and inflammation accompanying tissue damage (nociception). The VR-1 polynucleotide is useful for influencing the electrophysiological and/or pharmacological properties of a cell, and is also useful in the gene therapy treatment of disorders associated with sensory neurons and/or cells of the immune system and also for the preparation of a medicament for use in gene therapy. The VR-1 polynucleotides and polypeptides are useful for identifying a substance with ion-channel modulating activity (such as analgesics), or compounds which affect nociception, immunomodulatory agents, neuromodulatory agents.

Sequence 2765 BP; 560 A; 821 C; 792 G; 589 T; 3 other;

Query Match	54.3%	Score 1340;	DB 21;	Length 2765;
Best Local Similarity	99.1%	Pred. No. 0;		
Matches 2440;	Conservative 0;	Mismatches 22;	Indels 0;	Gaps 0;

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Db	749	tcaaatgacctgattctctgcacactgtctgaaagatcgaaacagggaaatctctgcaatctcaagccc	800
QY	548	tgtgtaaatgcccagatvgaaacagatgaatcaattaccgaaagaccaaagccgctctgaaatctgca	607
Db	809	tgtgtaaatgcccagatvgaaacagatgaatcaattaccgaaagaccaaagccgctctgaaatctgca	868
QY	608	ttagaaagaaagaaagatctctcagatgtgtgaaagatccctcgtgtgaaagaaatvgggccaatgtctgacg	667
Db	869	ttagaaagaaagaaagatctctcagatgtgtgaaagatccctcgtgtgaaagaaatvgggccaatgtctgacg	928

QY 668 cccgggctgagcgctctctccagaagggcagaaggaatttatttcgtgagc 727
DB 929 cccgggctgagcgctctctccagaagggcagaaggaatttatttcgtgagc 988
QY 728 taaccctctcttgagcgcttgcaacaagcagtggaattgtgtaagctacccctggaga 787
DB 989 taaccctctcttgagcgcttgcaacaagcagtggaattgtgtaagctacccctggaga 1048
QY 788 acccaacaacagcccgccagcctgcaagggcactgactcccaagggaacaacagctgcatg 847
DB 1049 acccaacaacagcccgccagcctgcaagggcactgactcccaagggaacaacagctgcatg 1108
QY 848 cccctggtgattgtcttcgagcaactcagctggaagaacattgtgactgtgacagcatgtatg 907
DB 1109 cccctggtgattgtcttcgagcaactcagctggaagaacattgtgactgtgacagcatgtatg 1168
QY 908 atgggctcctccaaagctggggccgctctgcccatacgtgagcttgagagcatccgca 967
DB 1169 atgggctcctccaaagctggggccgctctgcccatacgtgagcttgagagcatccgca 1228
QY 968 accctgagatctcagcgcctctgaaagtggccgcaaggggcaagatcgaatttca 1027
DB 1229 accctgagatctcagcgcctctgaaagtggccgcaaggggcaagatcgaatttca 1288
QY 1028 ggcacatctctgagcgaggagtttcaagactgagccacccctccgaaagtccacggagt 1087
DB 1289 ggcacatctctgagcgaggagtttcaagactgagccacccctccgaaagtccacggagt 1348
QY 1088 ggtgctatgggagctgtccggggtgctgctgtaagactgctgtgtgagagctgtgagg 1147
DB 1349 ggtgctatgggagctgtccggggtgctgctgtaagactgctgtgtgagagctgtgagg 1408
QY 1148 agaactcagtgctgagagatcattgctcttcaattgcaagagcccgcaacgcaacgaatgg 1207
DB 1409 agaactcagtgctgagagatcattgctcttcaattgcaagagcccgcaacgcaacgaatgg 1468
QY 1208 tggtttggagcccttgaaacaacactgctgcaagggcaaatggatctgctatcccaagt 1267
DB 1469 tggtttggagcccttgaaacaacactgctgcaagggcaaatggatctgctatcccaagt 1528
QY 1268 tcttcttaactctctggtatctgatactgatactgatacttcaacgctgtgtgctacc 1327
DB 1529 tcttcttaactctctggtatctgatactgatactgatacttcaacgctgtgtgctacc 1588
QY 1328 atcagcctacccctgaaagaagcagggccgcccctcaacctgaaagcgaggtttgaaactca 1387
DB 1589 atcagcctacccctgaaagaagcagggccgcccctcaacctgaaagcgaggtttgaaactca 1648
QY 1388 tgcgtctgagcgagcaactccttactcgtcaggggagatcactcctcgttggcgacg 1447
DB 1649 tgcgtctgagcgagcaactccttactcgtcaggggagatcactcctcgttggcgacg 1708
QY 1448 tgtgtatcttctggcgagcgagctgtcatctgatactgttataagaagctactttg 1507
DB 1709 tgtgtatcttctggcgagcgagctgtcatctgatactgttataagaagctactttg 1768
QY 1508 aaatcctctctcgttccagggccctgctcagacagtggtgtcccaaggtgctgtttccctg 1567
DB 1769 aaatcctctctcgttccagggccctgctcagacagtggtgtcccaaggtgctgtttccctg 1828
QY 1568 ccattcgagtgtagctcctcctcgttgtgtcgtcgtggtgctggtgctgtagaactgc 1627
DB 1829 ccattcgagtgtagctcctcctcgttgtgtcgtcgtggtgctggtgctgtagaactgc 1888
QY 1628 tttaactatacagctgctcagacacagggcatctacaggtatcatcagaaggttca 1687
DB 1889 tttaactatacagctgctcagacacagggcatctacaggtatcatcagaaggttca 1948
QY 1688 tctctgaggaactcgtcgtcctctctctgatactactagcttctccttgcgtcgtg 1747
DB 1949 tctctgaggaactcgtcgtcctctctctgatactactagcttctccttgcgtcgtg 2008

QY 1748 tagccctgtgagcctgagccaggaagcttggcgcccccgaagctctctacagggccccaag 1807
DB 2009 tagccctgtgagcctgagccaggaagcttggcgcccccgaagctctctacagggccccaag 2068
QY 1808 ccacagagctcagtgagcccatggagggagcagaagagacgaagggcagcgggcccaataca 1867
DB 2069 ccacagagctcagtgagcccatggagggagcagaagagacgaagggcagcgggcccaataca 2128
QY 1868 ggggtatccttgaaagccctccttgagagctctcaaatctacacatccgcatggcgagcttg 1927
DB 2129 ggggtatccttgaaagccctccttgagagctctcaaatctacacatccgcatggcgagcttg 2188
QY 1928 ccttccaggaagcagctgcaactcccgagatggtgtcgtctgtcgtcgtcgtcgtcgtcgtc 1987
DB 2189 ccttccaggaagcagctgcaactcccgagatggtgtcgtctgtcgtcgtcgtcgtcgtcgtc 2248
QY 1988 tgcatacctaaactcctcgtcgtcgaacatgctatgctgctcctatgagcgagcgtcaaca 2047
DB 2249 tgcatacctaaactcctcgtcgtcgaacatgctatgctgctcctatgagcgagcgtcaaca 2308
QY 2048 ggtcgcacactgacagctgagcagctggaagctgcaagaagccatctcgtccttgagga 2107
DB 2309 ggtcgcacactgacagctgagcagctggaagctggaagctgcaagaagccatctcgtccttgagga 2368
QY 2108 tggagaatggtctattgtgtgtgaggaagcagcgaggtgtgagatgctgagcagctgtg 2167
DB 2369 tggagaatggtctattgtgtgtgaggaagcagcgaggtgtgagatgctgagcagctgtg 2428
QY 2168 gacactaaagccagatgagcagccggatgagcgtgtgtcctcaggggtgagagagtgaaact 2227
DB 2429 gacactaaagccagatgagcagccggatgagcgtgtgtcctcaggggtgagagagtgaaact 2488
QY 2228 gggcttcttgaggaagcagcgtcgtcagctgtgtgaggaagccggtcaggggaggtgtcc 2287
DB 2489 gggcttcttgaggaagcagcgtcgtcagctgtgtgaggaagccggtcaggggaggtgtcc 2548
QY 2288 ctggaactctgaggaagcctgtcctggtctcccccgaaggaagatgagatgtgctc 2347
DB 2549 ctggaactctgaggaagcctgtcctggtctcccccgaaggaagatgagatgtgctc 2608
QY 2348 ctggagaaactatgtgcgctcagcgtcctccacagctcgaactgagtgccagatgacga 2407
DB 2609 ctggagaaactatgtgcgctcagcgtcctccacagctcgaactgagtgccagatgacga 2668
QY 2408 ggaagccagagagacagagagatcttccaaacacatcgtcgtcgttgggttccca 2467
DB 2669 ggaagccagagagacagagagatcttccaaacacatcgtcgtcgttgggttccca 2728
QY 2468 gt 2469
DB 2729 gt 2730

RESULT 8
AAV59691
ID AAV59691 standard; DNA; 2779 BP.
XX
AC AAV59691;
XX
DT 19-JAN-1999 (first entry)
DE Human secreted protein gene 181 clone HAFU18.
XX
KW Human; secreted protein; fusion protein; gene therapy; protein therapy;
diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia;
developmental abnormality; foetal deficiency; blood; allergy; renal; ds;
immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma;
inflammation; ischemic shock; Alzheimer's disease; restenosis; AIDS;
cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus;
osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion;
endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.
XX Homo sapiens.
OS

CC Interact with the novel capsaicin receptor VR1 (see AAY06558). The
 CC invention provides capsaicin receptor and capsaicin receptor.
 CC related polypeptides and polynucleotides, as well as expression
 CC vectors, host cells and transgenic animals. It also provides a
 CC method of using such receptors to identify vanilloid compounds in
 CC natural products or to screen candidate compounds that modulate
 CC capsaicin receptor function for use as analgesics (vanilloid
 CC analogues, therapeutic antibodies, antisense oligonucleotides,
 CC capsaicin receptor-encoding polynucleotides for gene therapy),
 CC flavour-enhancing agents, etc. Capsaicin receptor-related
 CC polypeptides and specific antibodies can also be used for the
 CC diagnosis and treatment of human disease and pain.

SO Sequence 884 BP; 182 A; 247 C; 267 G; 181 T; 7 other;

Query Match 21.9%; Score 541; DB 20; Length 884;
 Best Local Similarity 99.6%; Pred. No. 1.3e-225;
 Matches 691; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1776 ttgggccccgaagctctctacagcccaatgcaagagtcagtgcagcccatgaggg 1835
 DB 149 ttgggccccgaagctctctacagcccaatgcaagagtcagtgcagcccatgaggg 208
 QY 1836 acag 1895
 DB 209 acag 268
 QY 1896 ctccaattcaccatgcagctagggcagagctgcctcccaagagagagagagagag 1955
 DB 269 ctccaattcaccatgcagctagggcagagctgcctcccaagagagagagagagag 328
 QY 1956 catgt 2015
 DB 339 catgt 388
 QY 2016 gctctcgcctcctcag 2075
 DB 389 gctctcgcctcctcag 448
 QY 2076 gaagctgag 2135
 DB 449 gaagctgag 508
 QY 2136 gaag 2195
 DB 509 gaag 568
 QY 2196 ggcgt 2255
 DB 569 ggcgt 628
 QY 2256 gctgt 2315
 DB 629 gctgt 688
 QY 2316 ttcccccctcccaag 2375
 DB 689 ttcccccctcccaag 748
 QY 2376 cctccacatccaactgag 2435
 DB 749 cctccacatccaactgag 808
 QY 2436 ttccaacacatctgt 2469
 DB 809 ttccaacacatctgt 842

RESULT 11
 AAX19741
 ID AAX19741 standard; DNA: 884 BP.
 XX

AC AAX19741;
 XX 16-JUN-1999 (first entry)
 DT
 XX Human VRP-1 (VR2) capsaicin receptor DNA sequence #3.
 DE
 XX
 KM VR1: capsaicin receptor; VR2; VRP-1; analgesic; diagnosis;
 KM human disease; painful syndrome; ss.
 XX
 OS Homo sapiens.
 XX
 PN W090909140-A1.
 XX
 PD 25-FEB-1999.
 XX
 PF 20-AUG-1998; 98WO-US17466.
 XX
 PR 22-JAN-1998; 98US-0072151.
 PR 20-AUG-1997; 97US-0915461.
 XX
 PA (REGC) UNIV CALIFORNIA.
 XX
 PI Brake A, Caterina M, Julius DJ;
 XX
 DR WPI; 1999-181023/15.
 XX
 PT New capsaicin receptor polypeptide - useful for screening or
 PS characterising capsaicin receptor-binding compounds
 XX
 PS Claim 8; Page 85-86; 99pp; English.
 XX
 CC The present sequence encodes an isolated capsaicin receptor polypeptide
 CC (1). Capsaicin polypeptides are useful for identifying binding compounds
 CC which affect cellular responses. Preferably this is for identifying a
 CC compound that binds (1) and affects a cellular response associated with
 CC capsaicin biological activity (e.g. intracellular calcium flux). The
 CC polypeptides and host cells are useful for detecting a vanilloid
 CC product (an essential structural component of capsaicin) from natural
 CC products by detecting an alteration of intracellular response associated
 CC with capsaicin receptor activity, preferably an alteration of
 CC intracellular calcium levels, and are useful for screening for compounds
 CC for use in analgesics. Capsaicin receptor polypeptides and antibodies
 CC are useful for diagnosis and treatment of human diseases and painful
 CC syndromes. The transgenic mammals can be used to screen for capsaicin
 CC receptor antagonists and agonists. Prior art methods for screening or
 CC characterising new capsaicin receptor-binding compounds relied on assays
 CC using sensory neurons in culture or in intact animals. The new
 CC polypeptides provide a more sensitive screen.
 XX
 SO Sequence 884 BP; 182 A; 247 C; 267 G; 181 T; 7 other;

Query Match 21.9%; Score 541; DB 20; Length 884;
 Best Local Similarity 99.6%; Pred. No. 1.3e-225;
 Matches 691; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1776 ttgggccccgaagctctctacagcccaatgcaagagtcagtgcagcccatgaggg 1835
 DB 149 ttgggccccgaagctctctacagcccaatgcaagagtcagtgcagcccatgaggg 208
 QY 1836 acag 1895
 DB 209 acag 268
 QY 1896 ctccaattcaccatgcagctagggcagagctgcctcccaagagagagagagagag 1955
 DB 269 ctccaattcaccatgcagctagggcagagctgcctcccaagagagagagagagag 328
 QY 1956 catgt 2015
 DB 329 catgt 388
 QY 2016 gctctcgcctcctcag 2075

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Db 389 gctctgccccccwagagcgagacccgtcaacagctgtccactgacaagctgagacatcg 448
Oy 2076 gaagctgcagaagaaccatctctgtccctgagagatggaatgtgctattgtgtgcagaa 2135
Db 449 gaagctgcagaagaaccatctctgtccctgagagatggaatgtgctattgtgtgcagaa 508
Oy 2136 gaagcagcgagcaggtgtgtatgtctaacgcttgcacataagccagatgtgagccgagatga 2195
Db 509 gaagcagcgagcaggtgtgtatgtctaacgcttgcacataagccagatgtgagccgagatga 568
Oy 2196 ggcgtggtgcttcacaggtgagaggaagtgaaactgagcttcacatgagagccagacgtctac 2255
Db 569 ggcgtggtgcttcacaggtgagaggaagtgaaactgagcttcacatgagagccagacgtctac 628
Oy 2256 gctgtgtgagagaccgttcagagggcagctgtctccctgaaactccgagaaaccgtctgagc 2315
Db 629 gctgtgtgagagaccgttcagagggcagctgtctccctgaaactccgagaaaccgtctgagc 688
Oy 2316 ttccctcccaagagagatgagatgtgctctcagagaaactgtgtccgctcagct 2375
Db 689 ttccctcccaagagagatgagatgtgctctcagagaaactgtgtccgctcagct 748
Oy 2376 cctcagctcacaactgtagtgcacagatgacagagagagccagagagacagagagatct 2435
Db 749 cctcagctcacaactgtagtgcacagatgacagagagagccagagagacagagagatct 808
Oy 2436 ttccaacacatctgctgtgctgtgggtccagct 2469
Db 809 ttccaacacatctgctgtgctgtgggtccagct 842

RESULT 12
AA207115
ID AA207115 standard; CDNA: 885 BP.
AC AA207115;
XX
XX 08-OCT-1999 (first entry)
XX
DE Human vanilloid receptor homologue VANILREP2 cDNA derived from ESTs.
XX
XX Human; vanilloid receptor homologue; VANILREP2; polymorphic variant;
XX PVP-1; therapy; diagnosis; chronic pain; neuropathic; postoperative;
XX rheumatoid arthritis; neuralgia; algesia; nerve injury; ischaemia;
XX neurodegeneration; stroke; incontinence; inflammatory disorder; ss.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX CDS 22..673
XX FT /*tag= a
XX FT /product= "VANILREP2"
XX FT /transl_except= (pos:133..135;aa:Xaa)
XX FT /note= "Xaa- unspecified"
XX FT /transl_except= (pos:139..141;aa:Xaa)
XX FT /note= "Xaa- unspecified"
XX FT /transl_except= (pos:148..150;aa:Lys)
XX FT /note= "this codon has an apparent 1 nucleotide
XX FT insertion which alters the reading frame"
XX FT /transl_except= (pos:470..472;aa:Tyr)
XX FT /note= "no stop codon given"
XX
XX MO993765-A1.
XX
XX 29-JUL-1999.
XX
XX 25-JAN-1999; 99MO-EP00420.
XX
XX 20-JAN-1999; 99GB-0001209.
XX 27-JAN-1998; 98BP-0300549.
XX 26-OCT-1998; 98GB-0023421.

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XX
XX (SMIR ) SMITHKLINE BEECHAM PLC.
XX
XX Davis JB, Duckworth DM, Hayes PD;
XX
XX MPI: 1999-479049/40.
XX P-PSDB; AAI29470.
XX
XX New human vanilloid receptor homologues (VANILREP2)
XX
XX Claim 16; Page 33; 47pp; English.
XX
XX The present sequence encodes a human vanilloid receptor homologue,
XX designated VANILREP2, derived from EST (expressed sequence
XX tag) sequences. VANILREP2 can be used to diagnose disease or
XX susceptibility to disease related to expression or activity of
XX VANILREP2 polypeptides. VANILREP2 may be used to treat diseases
XX including pain, (for example chronic, neuropathic, postoperative,
XX rheumatoid arthritis), neuralgia, algesia, nerve injury, ischaemia,
XX neurodegeneration, stroke, incontinence, and inflammatory disorders.
XX
XX Sequence 885 BP; 184 A; 248 C; 267 G; 182 T; 4 other;
XX
XX
XX Query Match 21.9%; Score 541; DB 20; Length 885;
XX Best Local Similarity 99.6%; Pred. No. 1.3e-225;
XX Matches 691; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX
XX 1776 ttggcgccccgaagatcctctacagggcccaatgccaagatgtagtcagccatgagag 1835
XX 151 ttggcgccccgaagatcctctacagggcccaatgccaagatgtagtcagccatgagag 210
XX 1836 acaggaagacagagagcaacggggcccaatgacaaggggtatcctgtgaagcctcttgagct 1895
XX 211 acaaggaagacagagagcaacggggcccaatgacaaggggtatcctgtgaagcctcttgagct 270
XX 1896 ctccaattcaccatcgagcatggcgagctgagctcttcacagagagacagcttcacggc 1955
XX 271 ctccaattcaccatcgagcatggcgagctgagctcttcacagagagacagcttcacggc 330
XX 1956 catggtgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgct 2015
XX 331 catggtgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgct 390
XX 2016 gctatgccttcataagacagagacccgttcaacagtgctgcacatgacacgtgagacatgt 2075
XX 391 gctatgccttcataagacagagacccgttcaacagtgctgcacatgacacgtgagacatgt 450
XX 2076 gaagctgcagaagaaccatctctgtcctgagagatgagagatgctattgtgtgagaa 2135
XX 451 gaagctgcagaagaaccatctctgtcctgagagatgagagatgctattgtgtgagaa 510
XX 2136 gaagcagcgagcaggtgtgtatgtctaacgcttgcacataagccagatgtgagccgagatga 2195
XX 511 gaagcagcgagcaggtgtgtatgtctaacgcttgcacataagccagatgtgagccgagatga 570
XX 2196 ggcgtggtgcttcacaggtgagaggaagtgaaactgagcttcacatgagagccagacgtctac 2255
XX 571 ggcgtggtgcttcacaggtgagaggaagtgaaactgagcttcacatgagagccagacgtctac 630
XX 2256 gctgtgtgagagaccgttcagagggcagctgtctccctgaaactccgagaaaccgtctgagc 2315
XX 631 gctgtgtgagagaccgttcagagggcagctgtctccctgaaactccgagaaaccgtctgagc 690
XX 2316 ttccctcccaagagagatgagatgtgctctcagagaaactatgtgtccgctcagct 2375
XX 691 ttccctcccaagagagatgagatgtgctctcagagaaactatgtgtccgctcagct 750
XX 2376 cctcagctcacaactgtagtgcacagatgacagagagagccagagagacagagagagatct 2435
XX 751 cctcagctcacaactgtagtgcacagatgacagagagagccagagagacagagagagatct 810
XX 2436 ttccaacacatctgctgtgctgtgggtccagct 2469

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Db 811 ttccaacacatctgctgctcgtcgggtccagc 844

RESULT 13

AAV59807

ID AAV59807 standard; DNA; 2860 BP.

AAV59807;

19-JAN-1999 (first entry)

Human secreted protein gene 181 clone HAFNU18.

Human, secreted protein; fusion protein; gene therapy; protein therapy; diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia; developmental abnormality; foetal deficiency; blood; allergy; renal; ds; immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma; inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS; cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus; osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion; endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.

Homo sapiens.

MO9839448-A2.

11-SEP-1998.

06-MAR-1998; 98WO-US04493.

02-OCT-1997; 97US-0061060.

07-MAR-1997; 97US-0038621.

07-MAR-1997; 97US-0040161.

07-MAR-1997; 97US-0040162.

07-MAR-1997; 97US-0040163.

07-MAR-1997; 97US-0040333.

07-MAR-1997; 97US-0040334.

07-MAR-1997; 97US-0040336.

07-MAR-1997; 97US-0040626.

11-APR-1997; 97US-0043311.

11-APR-1997; 97US-0043312.

11-APR-1997; 97US-0043313.

11-APR-1997; 97US-0043314.

11-APR-1997; 97US-0043558.

11-APR-1997; 97US-0043559.

11-APR-1997; 97US-0043576.

11-APR-1997; 97US-0043578.

11-APR-1997; 97US-0043580.

11-APR-1997; 97US-0043582.

11-APR-1997; 97US-0043670.

11-APR-1997; 97US-0043671.

11-APR-1997; 97US-0043672.

11-APR-1997; 97US-0043674.

23-MAY-1997; 97US-0047492.

23-MAY-1997; 97US-0047500.

23-MAY-1997; 97US-0047501.

23-MAY-1997; 97US-0047502.

23-MAY-1997; 97US-0047503.

23-MAY-1997; 97US-0047581.

23-MAY-1997; 97US-0047582.

23-MAY-1997; 97US-0047583.

23-MAY-1997; 97US-0047584.

23-MAY-1997; 97US-0047585.

23-MAY-1997; 97US-0047586.

23-MAY-1997; 97US-0047587.

23-MAY-1997; 97US-0047588.

23-MAY-1997; 97US-0047589.

23-MAY-1997; 97US-0047590.

23-MAY-1997; 97US-0047592.

23-MAY-1997; 97US-0047593.

23-MAY-1997; 97US-0047594.

23-MAY-1997; 97US-0047595.

PR 23-MAY-1997; 97US-0047596.
 PR 23-MAY-1997; 97US-0047597.
 PR 23-MAY-1997; 97US-0047598.
 PR 23-MAY-1997; 97US-0047599.
 PR 23-MAY-1997; 97US-0047600.
 PR 23-MAY-1997; 97US-0047601.
 PR 23-MAY-1997; 97US-0047612.
 PR 23-MAY-1997; 97US-0047613.
 PR 23-MAY-1997; 97US-0047614.
 PR 23-MAY-1997; 97US-0047615.
 PR 23-MAY-1997; 97US-0047617.
 PR 23-MAY-1997; 97US-0047618.
 PR 23-MAY-1997; 97US-0047632.
 PR 23-MAY-1997; 97US-0047633.
 PR 06-JUN-1997; 97US-0048964.
 PR 06-JUN-1997; 97US-0048974.
 PR 13-JUN-1997; 97US-0049610.
 PR 08-JUL-1997; 97US-0051926.
 PR 16-JUL-1997; 97US-0052872.
 PR 18-AUG-1997; 97US-0055724.
 PR 22-AUG-1997; 97US-0056630.
 PR 22-AUG-1997; 97US-0056631.
 PR 22-AUG-1997; 97US-0056632.
 PR 22-AUG-1997; 97US-0056636.
 PR 22-AUG-1997; 97US-0056637.
 PR 22-AUG-1997; 97US-0056662.
 PR 22-AUG-1997; 97US-0056664.
 PR 22-AUG-1997; 97US-0056845.
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 PR 22-AUG-1997; 97US-0056864.
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 PR 22-AUG-1997; 97US-0056875.
 PR 22-AUG-1997; 97US-0056876.
 PR 22-AUG-1997; 97US-0056877.
 PR 22-AUG-1997; 97US-0056878.
 PR 22-AUG-1997; 97US-0056879.
 PR 22-AUG-1997; 97US-0056880.
 PR 22-AUG-1997; 97US-0056881.
 PR 22-AUG-1997; 97US-0056882.
 PR 22-AUG-1997; 97US-0056884.
 PR 22-AUG-1997; 97US-0056886.
 PR 22-AUG-1997; 97US-0056887.
 PR 22-AUG-1997; 97US-0056888.
 PR 22-AUG-1997; 97US-0056889.
 PR 22-AUG-1997; 97US-0056892.
 PR 22-AUG-1997; 97US-0056893.
 PR 22-AUG-1997; 97US-0056894.
 PR 22-AUG-1997; 97US-0056903.
 PR 22-AUG-1997; 97US-0056908.
 PR 22-AUG-1997; 97US-0056909.
 PR 22-AUG-1997; 97US-0056910.
 PR 22-AUG-1997; 97US-0056911.
 PR 05-SEP-1997; 97US-0057650.
 PR 05-SEP-1997; 97US-0057659.
 PR 05-SEP-1997; 97US-0057761.
 PR 12-SEP-1997; 97US-0058785.

(HUMA-) HUMAN GENOME SCI INC.
 XX PA
 XX PI Bednarik DP, Brewer LA, Carter KC, Duan R, Ebner R, Endress GA;
 PI Feng P, Ferris AM, Fischer CL, Florence KA, Greene JM, Hu JS;
 PI Kyaw H, Lafleur DW, Li Y, Moore PA, Ni J, Olsen HS, Rosen CA;
 PI Ruben SM, Shi Y, Soppet DR, Young PE, Yu GL, Zeng Z;
 XX
 DR WFI: 1998-506364/43.
 DR P-PSDB: AAW75021.
 XX
 PT New isolated human genes and the secreted polypeptide(s) they encode
 PT - useful for diagnosis and treatment of e.g. cancers, neurological
 PT disorders, immune diseases, inflammation or blood disorders
 XX
 PS Claim 1; Page 538-539; 721pp: English.

XX This sequence represents a nucleic acid molecule designated Gene 181
 CC from the human cDNA clone HAFU18 (deposited as clone ATCC 97904 and
 CC ATCC 209050) which encodes a secreted human protein. The gene can be
 CC used to generate fusion proteins by linking to the gene to a human
 CC immunoglobulin Fc portion (e.g. AAV59502) for increasing the stability of
 CC the fused protein as compared to the human protein only.
 CC The invention relates to 186 novel genes and their fragments (nucleic
 CC acid sequences: AAV59511-V59812; amino acid sequences AAV74731-W75026)
 CC which are useful for preventing, treating or ameliorating medical
 CC conditions e.g. by protein or gene therapy. Also, pathological
 CC conditions can be diagnosed by determining the amount of the new
 CC polypeptides in a sample or by determining the presence of mutations in
 CC the new polynucleotides. Specific uses are described for each of the 186
 CC polynucleotides, based on which tissues they are most highly expressed in
 CC (see AAV59511 for described uses).

SO Sequence 2860 BP; 604 A; 834 C; 815 G; 587 T; 20 other;

Query Match 20.6%; Score 508; DB 19; Length 2860;

Best Local Similarity 100.0%; Pred. No. 2,6e-211; Mismatches 0; Indels 0; Gaps 0;

Matches 508; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 935 tctgctaccgtgacgttgaagacatcgcaacctgacagatctcagcctctgaagc 994
 DB 1265 tctgctaccgtgacgttgaagacatcgcaacctgacagatctcagcctctgaagc 1324
 QY 995 tggcgccgaaggaagggaagatcgaagatttcgaagcaatctcgaagggaatttcag 1054
 DB 1325 tggcgccgaaggaagggaagatcgaagatttcgaagcaatctcgaagggaatttcag 1384
 QY 1055 gactgaaccacaccttcccgaaagatccacgagtggtgtatggcctctccgggtgtcgc 1114
 DB 1385 gactgaaccacaccttcccgaaagatccacgagtggtgtatggcctctccgggtgtcgc 1444
 QY 1115 tgtatgacctggtctctgtgacagcgtggaagaaactcagctgagatctatgctt 1174
 DB 1445 tgtatgacctggtctctgtgacagcgtggaagaaactcagctgagatctatgctt 1504
 QY 1175 ttcatctcaagagccgcgcacacgacgaatggtcgttttggaaacctctgacaacacgc 1234
 DB 1505 ttcatctcaagagccgcgcacacgacgaatggtcgttttggaaacctctgacaacacgc 1564
 QY 1235 tgcagggaaatgggaatctctcatcccaagtctctcttaactctctgtaactcga 1294
 DB 1565 tgcagggaaatgggaatctctcatcccaagtctctcttaactctctgtaactcga 1624
 QY 1295 tctacatgctcatctctacagcgtgttgcctacacacagcctacccctgaagaagagccg 1354
 DB 1625 tctacatgctcatctctacagcgtgttgcctacacacagcctacccctgaagaagagccg 1684
 QY 1355 cccctccacccgaagagcgaggttggaaatccatgctgctgagagcgacacatctatcc 1414
 DB 1685 cccctccacccgaagagcgaggttggaaatccatgctgctgagagcgacacatctatcc 1744
 QY 1415 tgcctaggggagatctacatctctcgtgag 1442
 DB 1745 tgcctaggggagatctacatctctcgtgag 1772

RESULT 14

AAV59808 standard; DNA; 876 BP.

AAV59808;

19-JAN-1999 (first entry)

Human secreted protein gene 181 clone HAFU18.

Human; secreted protein; fusion protein; gene therapy; protein therapy;
 diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukemia;

KW developmental abnormality; foetal deficiency; blood; allergy; renal; ds;
 KW immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma;
 KW inflammation; ischaemic shock; Alzheimer's disease; resenosis; AIDS;
 KW cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus;
 KW osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion;
 KW endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.
 OS Homo sapiens.
 PN W09839448-A2.
 PD 11-SEP-1998.
 PF 06-MAR-1998;
 XX 98WO-US04493.
 PR 02-OCT-1997; 97US-0061060.
 PR 07-MAR-1997; 97US-0038621.
 PR 07-MAR-1997; 97US-0040161.
 PR 07-MAR-1997; 97US-0040162.
 PR 07-MAR-1997; 97US-0040163.
 PR 07-MAR-1997; 97US-0040333.
 PR 07-MAR-1997; 97US-0040334.
 PR 07-MAR-1997; 97US-0040336.
 PR 11-APR-1997; 97US-0040626.
 PR 11-APR-1997; 97US-0043311.
 PR 11-APR-1997; 97US-0043312.
 PR 11-APR-1997; 97US-0043313.
 PR 11-APR-1997; 97US-0043314.
 PR 11-APR-1997; 97US-0043558.
 PR 11-APR-1997; 97US-0043559.
 PR 11-APR-1997; 97US-0043576.
 PR 11-APR-1997; 97US-0043578.
 PR 11-APR-1997; 97US-0043580.
 PR 11-APR-1997; 97US-0043669.
 PR 11-APR-1997; 97US-0043670.
 PR 11-APR-1997; 97US-0043671.
 PR 11-APR-1997; 97US-0043672.
 PR 11-APR-1997; 97US-0043674.
 PR 23-MAY-1997; 97US-0047492.
 PR 23-MAY-1997; 97US-0047500.
 PR 23-MAY-1997; 97US-0047501.
 PR 23-MAY-1997; 97US-0047502.
 PR 23-MAY-1997; 97US-0047503.
 PR 23-MAY-1997; 97US-0047581.
 PR 23-MAY-1997; 97US-0047582.
 PR 23-MAY-1997; 97US-0047583.
 PR 23-MAY-1997; 97US-0047584.
 PR 23-MAY-1997; 97US-0047585.
 PR 23-MAY-1997; 97US-0047586.
 PR 23-MAY-1997; 97US-0047587.
 PR 23-MAY-1997; 97US-0047588.
 PR 23-MAY-1997; 97US-0047589.
 PR 23-MAY-1997; 97US-0047590.
 PR 23-MAY-1997; 97US-0047592.
 PR 23-MAY-1997; 97US-0047593.
 PR 23-MAY-1997; 97US-0047594.
 PR 23-MAY-1997; 97US-0047595.
 PR 23-MAY-1997; 97US-0047596.
 PR 23-MAY-1997; 97US-0047597.
 PR 23-MAY-1997; 97US-0047598.
 PR 23-MAY-1997; 97US-0047599.
 PR 23-MAY-1997; 97US-0047600.
 PR 23-MAY-1997; 97US-0047601.
 PR 23-MAY-1997; 97US-0047612.
 PR 23-MAY-1997; 97US-0047613.
 PR 23-MAY-1997; 97US-0047614.
 PR 23-MAY-1997; 97US-0047615.
 PR 23-MAY-1997; 97US-0047617.
 PR 23-MAY-1997; 97US-0047618.
 PR 23-MAY-1997; 97US-0047632.
 PR 23-MAY-1997; 97US-0047633.
 PR 06-JUN-1997; 97US-0048964.
 PR 06-JUN-1997; 97US-0048974.

[illegible]

Search completed: October 4, 2001, 11:17:39
Job time: 7624 sec

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FH Key Location/Qualifiers
FT CDS 41..350
FT /*tag= a
PN MO9937675-A1.
XX
XX 29-JUL-1999.
XX
XX 22-JAN-1999; 99MO-US01418.
XX
XX 22-JAN-1998; 98US-0072151.
XX
XX (REGC ) UNIV CALIFORNIA.
XX
XX Brake AJ, Caterina M, Julius DJ;
XX
XX WPI; 1999-469113/39.
XX
XX
XX New isolated capsaicin receptor polypeptide and related nucleic acid
XX - useful for detecting vanilloid compounds, identifying modulators,
XX and in diagnosis or treatment of e.g. pain and inflammation
XX
XX Claim 8; Page 87-88; 120pp; English.
XX
XX This is the nucleotide sequence of a human vanilloid receptor-
XX related polypeptide 1 (VRP-1 or VR2) partial cDNA. It codes for
XX the N-terminal region of a claimed VRP-1 polypeptide (see AY06560).
XX VRP-1 is an example of a capsaicin receptor-related polypeptide of
XX the invention. It is not activated by capsaicin or heat, but may
XX interact with the novel capsaicin receptor VR1 (see AY06558). The
XX invention provides capsaicin receptor and capsaicin receptor-
XX related polypeptides and polynucleotides, as well as expression
XX vectors, host cells and transgenic animals. It also provides a
XX method of using such receptors to identify vanilloid compounds in
XX natural products or to screen candidate compounds that modulate
XX capsaicin receptor function for use as analgesics (vanilloid
XX analogues, therapeutic antibodies, antisense oligonucleotides,
XX capsaicin receptor-encoding polynucleotides for gene therapy),
XX flavour-enhancing agents, etc. Capsaicin receptor-related
XX polypeptides and specific antibodies can also be used for the
XX diagnosis and treatment of human disease and pain.
XX
XX
XX Sequence 350 BP; 82 A; 97 C; 103 G; 65 T; 3 other:
XX
XX
XX Query Match 13.3%; Score 329; DB 20; Length 350;
XX Best Local Similarity 100.0%; Pred. No. 1.9e-133;
XX Matches 329; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 78 gcagctctctctctcctagatgacccaacctccagctctccagtttcaggttgagac 137
XX |||||||
XX 22 gcagctctctctctcctagatgacccaacctccagctctccagtttcaggttgagac 81
XX
XX 138 attagatggaggccaagaatgctctgaggcggaagaggaagctgatttggag 197
XX |||||||
XX 82 attagatggaggccaagaatgctctgaggcggaagaggaagctgatttggag 141
XX
XX 198 cgggctgcctccatgagtcacagttccaggcggaagacccaattcccccacagat 257
XX |||||||
XX 142 cgggctgcctccatgagtcacagttccaggcggaagacccaattcccccacagat 201
XX
XX 258 aagatgcaactcaactaccgaaggaagagtgccagtcagccggaaccgaacgatt 317
XX |||||||
XX 202 aagatgcaactcaactaccgaaggaagagtgccagtcagccggaaccgaacgatt 261
XX
XX 318 tgacccagatcggtcttcaatcggtctccggggtgtcccgagagatctgctgact 377
XX |||||||
XX 262 tgacccagatcggtcttcaatcggtctccggggtgtcccgagagatctgctgact 321
XX
XX 378 tccagagtaactgagcaagaccgaagat 406
XX |||||||
XX 322 tccagagtaactgagcaagaccgaagat 350

```

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: October 3, 2001, 17:33:47 ; Search time 30.95 Seconds
(without alignments)
3522.434 Million cell updates/sec

Title: US-09-445-614-2
Perfect score: 4376
Sequence: 1 MTPSSSPVFRLETLDDGQEE.....EDEDGASENNYVPVOLLQSN 824

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 425026 seqs, 132305027 residues

Total number of hits satisfying chosen parameters: 425026

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database: 1: SP archaea: *
2: SP bacteria: *
3: SP fungi: *
4: SP human: *
5: SP invertebrate: *
6: SP mammal: *
7: SP rhnc: *
8: SP organelle: *
9: SP phage: *
10: SP plant: *
11: SP rodent: *
12: SP unclassified: *
13: SP vertebrate: *
14: SP virus: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	3964	90.6	764 4 Q9Y5S1	Q9Y5S1 homo sapien
2	3905	89.2	764 4 Q9Y670	Q9Y670 mus musculu
3	3119	71.3	756 11 Q9WTR1	Q9WTR1 mus musculu
4	3011.5	68.8	761 11 Q9WTD2	Q9WTD2 rattus norv
5	3001.5	68.6	761 11 Q9QYH8	Q9QYH8 rattus norv
6	2988.5	68.3	762 11 Q9JMT8	Q9JMT8 rattus norv
7	1628.5	37.2	839 4 Q9H304	Q9H304 homo sapien
8	1625.5	37.1	839 4 Q9H0G9	Q9H0G9 homo sapien
9	1621.5	37.1	839 4 Q9N074	Q9N074 homo sapien
10	1618	37.0	838 11 Q9J433	Q9J433 rattus norv
11	1618	37.0	838 11 Q9JMS7	Q9JMS7 rattus norv
12	1613.5	36.9	839 4 Q9NY22	Q9NY22 homo sapien
13	1430	32.7	871 4 Q9HBC0	Q9HBC0 homo sapien
14	1428.5	32.6	871 11 Q9ERZ8	Q9ERZ8 rattus norv
15	1427	32.6	852 13 Q9DRS3	Q9DRS3 gallus gall
16	1427	32.6	871 4 Q9HBA0	Q9HBA0 homo sapien
17	1421.5	32.5	871 11 Q9ES76	Q9ES76 mus musculu
18	1420.5	32.5	871 11 Q9EPK8	Q9EPK8 mus musculu
19	1415.5	32.3	871 11 Q9EQZ4	Q9EQZ4 mus musculu

20	1409.5	32.2	873 11 Q9ERZ7	Q9ERZ7 mus musculu
21	1408.5	32.2	778 11 Q9DM56	Q9DM56 rattus norv
22	1112.5	25.4	528 11 Q9Z182	Q9Z182 rattus norv
23	945.5	21.6	511 4 Q9H303	Q9H303 homo sapien
24	933	21.3	471 11 Q9JLM0	Q9JLM0 rattus norv
25	634	14.5	725 4 Q9H296	Q9H296 homo sapien
26	629	14.4	725 4 Q9H1D1	Q9H1D1 homo sapien
27	628	14.4	725 4 Q9H1D0	Q9H1D0 homo sapien
28	605.5	13.8	727 11 Q9R186	Q9R186 rattus norv
29	589	13.5	723 11 Q9JIP0	Q9JIP0 rattus norv
30	586	13.4	730 6 Q9XSM3	Q9XSM3 oryctolagus
31	584	13.3	723 11 Q9JTL2	Q9JTL2 rattus norv
32	579.5	13.2	729 4 Q9N0A5	Q9N0A5 homo sapien
33	462	10.6	769 5 Q9N3I9	Q9N3I9 caenorhabd1
34	440.5	10.1	729 11 Q9J3J0	Q9J3J0 mus musculu
35	417.5	9.5	750 5 Q9VUD5	Q9VUD5 drosophila
36	403.5	9.2	900 5 Q61220	Q61220 caenorhabd1
37	381.5	8.7	790 5 P90784	P90784 caenorhabd1
38	364	8.3	937 5 Q17469	Q17469 caenorhabd1
39	338	7.7	1123 5 Q9W3W0	Q9W3W0 drosophila
40	261	6.0	519 5 Q22374	Q22374 caenorhabd1
41	255	5.8	1913 5 Q9GRV5	Q9GRV5 caenorhabd1
42	223	5.1	1274 5 Q9VSG9	Q9VSG9 drosophila
43	222.5	5.1	981 6 P79100	P79100 bos taurus
44	222.5	5.1	1453 5 Q9VNR4	Q9VNR4 drosophila
45	221	5.1	914 5 Q9VHY7	Q9VHY7 drosophila

ALIGNMENTS

RESULT	1	PRELIMINARY:	PRT:	764 AA.
Q9Y5S1	1			
ID	Q9Y5S1			
AC	Q9Y5S1			
DT	01-NOV-1999 (TRENBLREL. 12, Created)			
DT	01-NOV-1999 (TRENBLREL. 12, Last sequence update)			
DT	01-MAR-2001 (TRENBLREL. 16, Last annotation update)			
DE	VANILLOID RECEPTOR-LIKE PROTEIN 1.			
GN	VR-1			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.			
OX	NCBI_TaxID:9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE-99215558; PubMed-10201375;			
RA	Caterina M.J., Rosen T.A., Tomlinaga M., Brake A.J., Julius D.;			
RT	"A capsaicin-receptor homologue with a high threshold for noxious heat."			
RL	Nature 398:436-441(1999).			
DR	EMBL, AF129112; AAD26363.1; -			
DR	InterPro; IPR002110; -			
DR	InterPro; IPR002111; -			
DR	Pfam; PF00023; ank; 3.			
DR	PROSITE; PS50088; ANK_REPEAT; 1.			
DR	PROSITE; PS50297; ANK_REPEAT_REGION; 1.			
DR	SMART; SM00248; ANK; 1.			
KW	Receptor.			
SQ	SEQUENCE 764 AA; 85980 MW; A73E3696E70F91E9.CRC64;			
Query Match	Best Local Similarity	90.6%; Score 3964; DB 4; Length 764;		
		92.7%; Pred. No. 5.4e-296;		
	Matches 764; Conservative	0; Mismatches 0; Indels 60; Gaps 1;		
QY	1 MTPSSSPVFRLETLDDGQEDGSEADRGKLDGSLPMEISQFQEDRKFAPQIRVNLNY 60			
DB				
DB	1 MTPSSSPVFRLETLDDGQEDGSEADRGKLDGSLPMEISQFQEDRKFAPQIRVNLNY 60			
QY				
QY	61 RKGTSASQPDPRFRDRDLFNVRVSRGVGAGATCTGCTGACTTCAGACTACTGAG 120			
DB				
DB	61 RKGTSASQPDPRFRDRDLFNVRVSRGVGAGATCTGCTGACTTCAGACTACTGAG 120			
	88			

```

OY 121 CAAGACGACGAGTACCTACCGACGACTCGEDLAGLPEYLSKTSKYLTDSSEYTBSTGKTCL 180
DB 89 -----EDLAGLPEYLSKTSKYLTDSSEYTBSTGKTCL 120
OY 181 MKAVLNKQGVNACILPLQIDRDSGNPOPLVNAOCTDYYRGHSAHLHAIEKRSIQCYK 240
DB 121 MKAVLNKQGVNACILPLQIDRDSGNPOPLVNAOCTDYYRGHSAHLHAIEKRSIQCYK 180
OY 241 LIVENGANVHARACGRFFQKGGTCYFEGELPLSLAACKTQMDVSYLLENHQPASLQA 300
DB 181 LIVENGANVHARACGRFFQKGGTCYFEGELPLSLAACKTQMDVSYLLENHQPASLQA 240
OY 301 TDSQNTVYHALVMSIDNSAENIALVTSMDGLQAGARLCPVQLEDIRNODLPLKL 360
DB 241 TDSQNTVYHALVMSIDNSAENIALVTSMDGLQAGARLCPVQLEDIRNODLPLKL 300
OY 361 AAKEGKIEIFRHILOREFSGLSHLSRKFTQMGCPYRVSILYDLASVDSCEENSYLEITIAF 420
DB 301 AAKEGKIEIFRHILOREFSGLSHLSRKFTQMGCPYRVSILYDLASVDSCEENSYLEITIAF 360
OY 421 HCKSPHRRHVMVLEPLNKLQAKMDLLIPKFLNFCNLIMYEFITAVAYHQPTLKKQA 480
DB 361 HCKSPHRRHVMVLEPLNKLQAKMDLLIPKFLNFCNLIMYEFITAVAYHQPTLKKQA 420
OY 481 PHLKAEGVNSMLTGHILLLGGLYLVQOLWYFMRHNFIMISFDSYFEILFEOALL 540
DB 421 PHLKAEGVNSMLTGHILLLGGLYLVQOLWYFMRHNFIMISFDSYFEILFEOALL 480
OY 541 TVSQVLCFLAIEWYLPPLVSALVGLMNLVYTRGFQHTGYISVMIQVILRDILRFL 600
DB 481 TVSQVLCFLAIEWYLPPLVSALVGLMNLVYTRGFQHTGYISVMIQVILRDILRFL 540
OY 601 IYLVLFEGFAVALVLSQEAHREAPRGPNATESVQPMGQDEGNGAQRIGLLEASLEL 660
DB 541 IYLVLFEGFAVALVLSQEAHREAPRGPNATESVQPMGQDEGNGAQRIGLLEASLEL 600
OY 661 FKFTTGMGELAFQEOHLHFGVLLLLAVLLTYLLMLLALMSEYNSVATDSWSIM 720
DB 601 FKFTTGMGELAFQEOHLHFGVLLLLAVLLTYLLMLLALMSEYNSVATDSWSIM 660
OY 721 KLOKAIIVLENGYWMCKKQKORAGVMTLVGKPDGSPDERKCFRVEEYNMAWSMOTLPT 780
DB 661 KLOKAIIVLENGYWMCKKQKORAGVMTLVGKPDGSPDERKCFRVEEYNMAWSMOTLPT 720
OY 781 LCEDPGAGVPTLENPLVLPKDEDEGASEENTVPVQLOSN 824
DB 721 LCEDPGAGVPTLENPLVLPKDEDEGASEENTVPVQLOSN 764

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RESULT 2

OY 670 PRELIMINARY; PRT: 764 AA.

AC OY 670;

DR 01-NOV-1999 (TREMBLrel. 12, Created)

DR 01-NOV-1999 (TREMBLrel. 12, Last sequence update)

DR 01-MAR-2001 (TREMBLrel. 16, Last annotation update)

DE VANILLOID RECEPTOR-LIKE PROTEIN.

GN

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

OX NCBI_TaxID=9606;

RY

RM

RA SEQUENCE FROM N. A.

RP Garcia R.L., Delmas P., Cesare P., England S., Liapi A., Wood J.N.;

RT "Cloning and functional expression of VRL, a vanilloid receptor-like

RT gene."

RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.

DR EMBL: AF103906; AAD1724.1; -

DR InterPro: IPR002110; -

DR InterPro: IPR002111; -

DR Pfam: PF00023; ank; 3.

```

DR PROSITE: PS50088; ANK_REPEAT; 1.
DR PROSITE: PS50297; ANK_REPEAT_REGION; 1.
DR SMART: SM00248; ANK; 1.
KW Receptor.
SQ SEQUENCE 764 AA; 86053 MW; AF0DE8F495E8A3A0 CRC64;

Query Match 89.2%; Score 3905; DB 4; Length 764;
Best Local Similarity 91.0%; Pred. No. 1.8e-291;
Matches 750; Conservative 6; Mismatches 8; Indels 60; Gaps 1;

OY 1 MTPSSSPVPRLETTLDGGQEDSGEADRGKLDGSGGLPPEMSQFQGEDRKFPAPQIRVNLNY 60
DB 1 MTPSSSPVPRLETTLDGGQEDSGEADRGKLDGSGGLPPEMSQFQGEDRKFPASQIRVNLNY 60
OY 61 RKGTGASQDPNRPDRDRFENAVSRGVPAAGATCGGCTGAGCTCCAGAGTACCTGAG 120
DB 61 RKGTGASQDPNRPDRDRFENAVSRGVPAAGATCGGCTGAGCTCCAGAGTACCTGAG 120
OY 121 CAAGACGACGAGTACCTACCGACGACTCGEDLAGLPEYLSKTSKYLTDSSEYTBSTGKTCL 180
DB 89 -----EDLAGLPEYLSKTSKYLTDSSEYTBSTGKTCL 120
OY 181 MKAVLNKQGVNACILPLQIDRDSGNPOPLVNAOCTDYYRGHSAHLHAIEKRSIQCYK 240
DB 121 MKAVLNKQGVNACILPLQIDRDSGNPOPLVNAOCTDYYRGHSAHLHAIEKRSIQCYK 180
OY 241 LIVENGANVHARACGRFFQKGGTCYFEGELPLSLAACKTQMDVSYLLENHQPASLQA 300
DB 241 LIVENGANVHARACGRFFQKGGTCYFEGELPLSLAACKTQMDVSYLLENHQPASLQA 300
OY 301 TDSQNTVYHALVMSIDNSAENIALVTSMDGLQAGARLCPVQLEDIRNODLPLKL 360
DB 301 TDSQNTVYHALVMSIDNSAENIALVTSMDGLQAGARLCPVQLEDIRNODLPLKL 360
OY 361 AAKEGKIEIFRHILOREFSGLSHLSRKFTQMGCPYRVSILYDLASVDSCEENSYLEITIAF 420
DB 361 AAKEGKIEIFRHILOREFSGLSHLSRKFTQMGCPYRVSILYDLASVDSCEENSYLEITIAF 420
OY 421 HCKSPHRRHVMVLEPLNKLQAKMDLLIPKFLNFCNLIMYEFITAVAYHQPTLKKQA 480
DB 421 HCKSPHRRHVMVLEPLNKLQAKMDLLIPKFLNFCNLIMYEFITAVAYHQPTLKKQA 480
OY 481 PHLKAEGVNSMLTGHILLLGGLYLVQOLWYFMRHNFIMISFDSYFEILFEOALL 540
DB 481 PHLKAEGVNSMLTGHILLLGGLYLVQOLWYFMRHNFIMISFDSYFEILFEOALL 540
OY 541 TVSQVLCFLAIEWYLPPLVSALVGLMNLVYTRGFQHTGYISVMIQVILRDILRFL 600
DB 541 TVSQVLCFLAIEWYLPPLVSALVGLMNLVYTRGFQHTGYISVMIQVILRDILRFL 600
OY 601 IYLVLFEGFAVALVLSQEAHREAPRGPNATESVQPMGQDEGNGAQRIGLLEASLEL 660
DB 601 IYLVLFEGFAVALVLSQEAHREAPRGPNATESVQPMGQDEGNGAQRIGLLEASLEL 660
OY 661 FKFTTGMGELAFQEOHLHFGVLLLLAVLLTYLLMLLALMSEYNSVATDSWSIM 720
DB 661 FKFTTGMGELAFQEOHLHFGVLLLLAVLLTYLLMLLALMSEYNSVATDSWSIM 720
OY 721 KLOKAIIVLENGYWMCKKQKORAGVMTLVGKPDGSPDERKCFRVEEYNMAWSMOTLPT 780
DB 721 KLOKAIIVLENGYWMCKKQKORAGVMTLVGKPDGSPDERKCFRVEEYNMAWSMOTLPT 780
OY 781 LCEDPGAGVPTLENPLVLPKDEDEGASEENTVPVQLOSN 824
DB 781 LCEDPGAGVPTLENPLVLPKDEDEGASEENTVPVQLOSN 764

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RESULT 3

OY 670 PRELIMINARY; PRT: 756 AA.

AC OY 670;

DR 01-NOV-1999 (TREMBLrel. 12, Created)

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DT 01-NOV-1999 (TRENBLREL. 12, Last sequence update)
DT 01-MAR-2001 (TRENBLREL. 16, Last annotation update)
DE GROWTH FACTOR REGULATED CALCIUM CHANNEL.
GN VRL1 OR GRC.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57 BLACK-6; TISSUE=SPLEEN;
RA Kanazaki M., Zhang Y., Kojima I.;
RT "Growth factor regulated calcium channel."
RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB021665; BAA78478.1;
DR MGD; MGI:1341836; Vrl1.
DR InterPro: IPR002110;
DR InterPro: IPR002111;
DR Pfam; PF00023; ank; 3.
DR PROSITE; PS50088; ANK_REPEAT; 1.
DR PROSITE; PS50297; ANK_REPEAT_REGION; 1.
DR SMART; SM00248; ANK; 1.
SQ SEQUENCE 756 AA; 85964 MW; 4C037D0F6066EFA4 CRC64;

Query Match          71.3%; Score 3119; DB 11; Length 756;
Best Local Similarity 74.5%; Pred. No. 4,1e-231;
Matches 615; Conservative 55; Mismatches 84; Indels 72; Gaps 6;

OY 1 MTSFSSPVFRLTLDGGQEDGSEADRGKLDGSGGLPPMESQFQGEDRKFAPQIRVNLNY 60
DB 1 MTSASNPPARLFETSDDEGSAEVNKKG---NEPPMESPFQEDRNFSPQIKVNLNY 56
OY 61 RKGGASQDPNFRDRDRLEFNARVSGVPGAGACTGGCTGACTCCAGACTACTGAG 120
DB 57 RKGGSPSQDPNFRDRDRLEFVSVRGP----- 84
OY 121 CAAGACGACGAGACTACTCCAGACTGAGLPEYLSTSKYLTDEYTEGSTGTCL 180
DB 85 -----EELTGLLELYRRSKYLTDSAYTEGSTGTCL 116
OY 181 MKAVLNTKQVNNACILPQLQIDRDSGNQPLVNAOCTDDYRGHSALHAIEKRSLOCVK 240
DB 117 MKAVLNTQDGVNACILPQLQIDRDSGNQPLVNAOCTDEFRGSHALHAIEKRSIMCVK 176
OY 241 LTVNGNANVHARACGRFFQKQCTCFEGELPLSLAACKQMDVSYLLENPHQPASLEA 300
DB 177 LTVNGNANVHARACGRFFQKQCTCFEGELPLSLAACKQMDVSYLLENPHQPASLEA 236
OY 301 TDSQGNVLAHALVAMISDSANENIALVTSMYDGLQAGARLCPVQLEDIRNLQDLPKL 360
DB 237 TDSQGNVLAHALVAMISDSANENIALVTSMYDGLQAGARLCPVQLEDIRNLQDLPKL 296
OY 361 AAKEGKLEIFRHIIQREPSGL-SHLSRKFTWCYGPVAVSLYDASVDSCEENSVLEIIA 419
DB 297 AAKEGKLEIFRHIIQREPSGL-SHLSRKFTWCYGPVAVSLYDASVDSCEENSVLEIIA 356
OY 420 FHCSPIRHRHVLEPIINKLQAKWDLIPREFLNFLCNLYMFLFAVAHOPLIKQOA 479
DB 357 FHCSPIRHRHVLEPIINKLQAKWDLIPREFLNFLCNLYMFLFAVAHOPLIKQOA 416
OY 480 APLHKAEGNSMLTGLHILLGLGIYLLVQGLWYFWRHRVFIWISFIDSYFEILFEQAL 539
DB 417 IPSKAFQSGSMILLGLHILLGLGIYLLGLQWYFWRHRVFIWISFIDSYFEILFEQAL 476
OY 540 LTVISQVLCFLAIVMYPLVLSALVGLMNLITYTRGFQHTGITSVMIQYILNDLRF 599
DB 477 LTVISQVLCFLAIVMYPLVLSALVGLMNLITYTRGFQHTGITSVMIQYILNDLRF 536
OY 600 LTVVLFEGFVALVLSLSOEAWRPEATGPAPATSVOPMEQDEGNAOVRGLILEASLE 659
DB 537 LTVVLFEGFVALVLSLSOEAWRPEATGPAPATSVOPMEQDEGNAOVRGLILEASLE 594
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OY 660 LFKFTIGGELAFQEQHFRGMVLLLLAYVLLIYLLLNMLIALMSTVNSVATDSMSI 719
DB 595 LFKFTIGGELAFQEQHFRGMVLLLLAYVLLIYLLLNMLIALMSTVNSVATDSMSI 654
OY 720 WKLOKAIVLEENGVNMYCKRKK--RAGVMLTVGTRKQDPSPERNCFRFEVNMASMEQTL 778
DB 655 WKLOKAIVLEENGVNMYCKRKKRHRGRLLVGTIGDGIPIERNCFRFEVNMAMAMEXTL 714
OY 779 PTLCEPAGVPTLNPVLASPEKEDGASEENYVPVOLLQSN 824
DB 715 PTLSDPAGAGITGKKKNT-----SKPKNSASEDHLPLVLOSH 756

RESULT 4
O9WUD2 PRELIMINARY; PRT: 761 AA.
AC O9WUD2:
DT 01-NOV-1999 (TRENBLREL. 12, Created)
DT 01-NOV-1999 (TRENBLREL. 12, Last sequence update)
DT 01-MAR-2001 (TRENBLREL. 16, Last annotation update)
DE VANILLOID RECEPTOR-LIKE PROTEIN 1.
GN VRL-1.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SPRAGUE-DAWLEY;
RA MEDLINE-99215558; PubMed-10201375;
RA Caterina M.J., Rosen T.A., Tominaga M., Brake A.J., Julius D.;
RT "A capsaicin-receptor homologue with a high threshold for noxious heat".
RL Nature 398:436-441(1999).
DR EMBL; AF129113; AAD26364.1;
DR InterPro: IPR002110;
DR InterPro: IPR002111;
DR Pfam; PF00023; ank; 3.
DR PROSITE; PS50088; ANK_REPEAT; 1.
DR PROSITE; PS50297; ANK_REPEAT_REGION; 1.
DR SMART; SM00248; ANK; 1.
DR KX Receptor.
SQ SEQUENCE 761 AA; 86689 MW; 46A281183EBE672F CRC64;

Query Match          68.8%; Score 3011.5; DB 11; Length 761;
Best Local Similarity 72.0%; Pred. No. 7,5e-223;
Matches 598; Conservative 62; Mismatches 93; Indels 77; Gaps 8;

OY 1 MTSFSSPVFRLTLDGGQEDGSEADRGKLDGSGGLPPMESQFQGEDRKFAPQIRVNLNY 60
DB 1 MTSASSPPARLFETSDDEGSAEVNKKQKQ---PPMESPFQEDRNFSPQIKVNLNY 56
OY 61 ---RKGTGA-SQDPNFRDRDRLEFNARVSGVPGAGATCTGGCTGACTCCAGACTAC 115
DB 57 IKRPPKNTSAPSQDEPDRDRLEFVSVRGP----- 89
OY 116 CTGACGACGACGACGACTACTCCAGACTGAGLPEYLSTSKYLTDEYTEGST 175
DB 90 -----EELTGLLELYLMNRSKYLTDSAYTEGST 116
OY 176 GKTCMLKAVNLKQVNNACILPQLQIDRDSGNQPLVNAOCTDDYRGHSALHAIEKRS 235
DB 117 GKTCMLKAVNLKQVNNACILPQLQIDRDSGNQPLVNAOCTDEFRGSHALHAIEKRS 176
OY 236 LQCYKLVENGANVHARACGRFFQKQCTCFEGELPLSLAACKQMDVSYLLENPHQ 295
DB 177 LQCYKLVENGADVHARACGRFFQKQCTCFEGELPLSLAACKQMDVSYLLENPHQ 236
OY 296 ASLQATDSQNTVLAHVMISDSANENIALVTSMYDGLQAGARLCPVQLEDIRNLQD 355
DB 237 ASLQATDSQNTVLAHVMISDSANENIALVTSMYDGLQAGARLCPVQLEDIRNLQD 296
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QY 356 TPRLKAAKGGKIEIRPHIIQORESG--LSHLSKRTFEMCGPVRVSLYDLASVDSCEENV 414
DB 297 TPRLKAAKGGKIEIRPHIIQORESGPYOPLSRKFTFEMCGPVRVSLYDLASVDSMEKNSV 356
QY 415 LEIIAFHCKSPRRHRNVLEPLNKLLOAKMDLLIPKFLNFCNLTYMFTFAVAAYHOPT 474
DB 357 LEIIAFHCKSPRRHRNVLEPLNKLLOAKMDLVSKFFENFACIYLYMFTFAVAAYHOPT 416
QY 475 LKQAPHLKAEVGNMGLTGHIILLGGIYLLVGLMFWRRHVFIMWISFIDSYEILF 534
DB 417 LDQPAIPSSKATFEGESMILLGHIILLGGIYLLVGLMFWRRHVFIMWISFIDSYEILF 476
QY 535 LFOALLTVSOVLCFLAIEWYPLVLSALVGLMNLITTRGFORTGISVMIQKYLND 594
DB 477 LFOALLTVSOVLCFLAIEWYPLVLSALVGLMNLITTRGFORTGISVMIQKYLND 536
QY 595 LIRFLIYLVLEFGFVALVLSLSOAMRPEAPTPGNATESVOPMEQDEGNAOYRGIL 654
DB 537 LIRFLIYLVLEFGFVALVLSLSREARSPKAPEDNNSTYDEPTYGQEE--PAPRSTL 594
QY 655 EASLELFFETIGMGLAFQEQDLHFRGMVLLLLAVYLLTYILLNKLALMSETVNSVAT 714
DB 595 DASLELFFETIGMGLAFQEQDLHFRGMVLLLLAVYLLTYILLNKLALMSETVNSVAT 654
QY 715 DMSIIMKLOKATSVLEMENGYMWC--RKKORAGVMLTVGCRKPGSPDERMCFVEEVNMA 773
DB 655 NMSIIMKLOKATSVLEMENGYMWCRRKKHREGRLKVGTRGQTPDERMCFVEEVNMA 714
QY 774 WEOTLPTLCEPSGAGVPTLENPVLASPKKEDGASEENTVYPOLLDS 823
DB 715 WEKTLPTLSEDBSGPITGNKNPT----SKRGKNSASEDHLPLOVLOS 760

RESULT 5
Q9QYH8 PRELIMINARY: PRT: 761 AA.
AC 09QYH8:
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAY-2001 (TREMBLrel. 16, Last annotation update)
DE STRETCH ACTIVATED CHANNEL 2B.
GN RSAC2B.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN (1)
RP SEQUENCE FROM N.A.
RA Ienhbaahl K.;
RT "Molecular cloning of a stretch activated channel from rat kidney.";
RT Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB029330; BAA8637.1; -.
DR InterPro: IPR002110; -.
DR InterPro: IPR002111; -.
DR Pfam: PF00023; ank. 3.
DR PROSITE: PS50088; ANK_REPEAT, 1.
DR PROSITE: PS50297; ANK_REPEAT_REGION, 1.
DR SMART; SM00248; ANK, 1.
SQ SEQUENCE 761 AA; 86705 MW; 89770CDEID5351EC8 CXC64;

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Query Match 68.6%; Score 3001.5; DB 11; Length 761;
 Best Local Similarity 71.9%; Pred. No. 4.4e-222;
 Matches 597; Conservative 62; Mismatches 94; Indels 77; Gaps 8;

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QY 1 MTSPPSPVFRLETLTGSGEDSGEADRGKLDGSGLPMESEFGQEDRKFAQIVNINLY 60
DB 1 MTSASSPPAFRLTSDGDEGNAEVNKGQEQ---PPPESEFQEDRRSSPOQIVNINLY 56
QY 61 ----RKGTGA-SQDPNFRDRDLRFNNAVSRGVGAGATCTGCTGAGACTCCAGATAC 115
DB 57 IKRPAPNTSAPSGQEPDRDRDLRFNNAVSRGV----- 89

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QY 116 CTGAGCAGACCAAGCAAGTACTCACCAGCTGEGDLAIPVLSKTSKYLTDSYETGST 175
DB 90 -----EELTGLLEYLRMNSKYLTDSAYETGST 116
QY 176 GRTCLMKAVLNKQGVNACITLLOTRDSGNPQPLVNNOCDDYRGSAHIAIEKRS 235
DB 117 GTCTLMKAVLNQDGVNACIMPLQIDKDSGNPKLLVNNOCDEFFQGHSAHIAIEKRS 176
QY 236 LOCVKLLVENGANVHARACGRFFQCGTGFEGELPLSLAECTOMDVSYLLENPHOP 295
DB 177 LOCVKLLVENGADVHARACGRFFQKHGCTGFEGELPLSLAECTOMDVSYLLENPHOP 236
QY 296 ASLQATDSQNTVLAHVLVISONSAENALVTSMTDGLLOAGARLCPTVOLEDIRNLQDL 355
DB 237 ASLEATDSQNTVLAHVLVIAIDNSPENSALVIMYDGLLOAGARLCPTVOLEIRSHQGL 296
QY 356 TPRLKAAKGGKIEIRPHIIQORESG--LSHLSKRTFEMCGPVRVSLYDLASVDSCEENV 414
DB 297 TPRLKAAKGGKIEIRPHIIQORESGPYOPLSRKFTFEMCGPVRVSLYDLASVDSMEKNSV 356
QY 415 LEIIAFHCKSPRRHRNVLEPLNKLLOAKMDLLIPKFLNFCNLTYMFTFAVAAYHOPT 474
DB 357 LEIIAFHCKSPRRHRNVLEPLNKLLOAKMDLVSKFFENFACIYLYMFTFAVAAYHOPT 416
QY 475 LKQAPHLKAEVGNMGLTGHIILLGGIYLLVGLMFWRRHVFIMWISFIDSYEILF 534
DB 417 LDQPAIPSSKATFEGESMILLGHIILLGGIYLLVGLMFWRRHVFIMWISFIDSYEILF 476
QY 535 LFOALLTVSOVLCFLAIEWYPLVLSALVGLMNLITTRGFORTGISVMIQKYLND 594
DB 477 LFOALLTVSOVLCFLAIEWYPLVLSALVGLMNLITTRGFORTGISVMIQKYLND 536
QY 595 LIRFLIYLVLEFGFVALVLSLSOAMRPEAPTPGNATESVOPMEQDEGNAOYRGIL 654
DB 537 LIRFLIYLVLEFGFVALVLSLSREARSPKAPEDNNSTYDEPTYGQEE--PAPRSTL 594
QY 655 EASLELFFETIGMGLAFQEQDLHFRGMVLLLLAVYLLTYILLNKLALMSETVNSVAT 714
DB 595 DASLELFFETIGMGLAFQEQDLHFRGMVLLLLAVYLLTYILLNKLALMSETVNSVAT 654
QY 715 DMSIIMKLOKATSVLEMENGYMWC--RKKORAGVMLTVGCRKPGSPDERMCFVEEVNMA 773
DB 655 NMSIIMKLOKATSVLEMENGYMWCRRKKHREGRLKVGTRGQTPDERMCFVEEVNMA 714
QY 774 WEOTLPTLCEPSGAGVPTLENPVLASPKKEDGASEENTVYPOLLDS 823
DB 715 WEKTLPTLSEDBSGPITGNKNPT----SKRGKNSASEDHLPLOVLOS 760

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RESULT 6
Q9JMI8 PRELIMINARY: PRT: 762 AA.
AC 09JMI8:
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE ION CHANNEL.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN (1)
RP SEQUENCE FROM N.A.
RA TISSUE=KIDNEY;
RA Suzuki M.;
RT "Ion channel.";
RT Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB022332; BAA93435.1; -.
DR InterPro: IPR002110; -.
DR InterPro: IPR002111; -.
DR Pfam: PF00023; ank. 3.
DR PROSITE: PS50088; ANK_REPEAT, 1.
DR PROSITE: PS50297; ANK_REPEAT_REGION, 1.

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DR SMART; SM00248; ANK; 1.  
SQ SEQUENCE 762 AA; 86767 MW; CE0970BC4195351E CRC64;
```

Query Match	68.3%	Score 2988.5	DB 11	length 762
Best local similarity	71.8%	Pred. No. 4.4e-221		
Matches 594	Conservative 62	Mismatches 94	Indels 77	Gaps 8

[illegible]

OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxId=9606;
RM
RM [1]
RP SEQUENCE FROM N.A.
RA Cortright D.N., Peck A., Zou T.;
RT "Cloning and characterization of the human capsacin receptor, VR1."
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF16175; AAC43466.1; -
KW Receptor
SQ SEQUENCE 839 AA; 94968 MW; EA9BF7D60235FF9F4 CRC64;

Query Match	37.2%	Score 1628.5	DB 4	Length 839
Best Local Similarity	48.8%	Pred. No. 1.4e-116		
Matches 339	Conservative 118	Mismatches 193	Indels 45	Gaps 11

ID	Q9H0G9	PRELIMINARY:	PRT:	839 AA.
QY	149	EDLGLPEYLSKTSYLLYSDSEYTESGTSKTCGLMKAVYLLKGVNAACILPILQIDRDSNP	20	
Db	128	QDESLELFLDKSKHLLDNENFEKDEGTCTLLKAMCLHHGQNTTLPILLEIARQDSTL	18	
QY	209	QPLVNAOCTDDYDYGSHSLHAIEKRSLOCYKLLVYENGANYHARACGRFEGGQ-TCFY	26	
Db	188	KELVNASYSDSYGQNTALHAIERNNALVTLLENADVDQAANHDFEKTGREGFY	24	
QY	268	FGEPLPSIAACTKQMDVSYLLENPHQPSLQATDSQGNVTVAALVMSISABNIALVT	32	
Db	248	FGEPLPSIAACTNOLGIVKFLQNSWQTAIDSADSQGNVTVAALVEADTADNTKFEVT	30	
QY	328	SMYGGILLQAGRLCPTVOLDEDIRNLQDTPLKLAKEGKIEIFPHILLORES--GLSHS	38	
Db	308	SMYDEILMLGKKHLPFLTKLEELYTKKGTPTALAAAGCKIVLAVYLQREIQEPECRLS	36	
QY	386	RKFTWCYGPVAVSLDYLDASVDSCEENSVLTEIIAF-HCKSPHRRMYVLEPLNKLQAKW	44	
Db	368	RKFTEMAAGPVHSLSDYDSCIDTCEKNSVLEVIAYSSESEPTNRHMDLVEPLNKLQAKW	42	
QY	445	DLILPK--PELLFCLNLVMTFTFAVAHOPPLKQAAPHKAE--VGNMSMLTGHILLG	50	
Db	428	DREVKRIEYFENFVLYCYMIIFTMAAAYRPV--DGLPPEKMEKIGDYFRVTGBILSVLG	48	
QY	503	GIVLLVQOLMFMRRHNFVWISFSDSEYFEELIFQALITVVSQVCLATEMYVPLLYSA	56	
Db	485	GIVYFFFGIOQFLDORRSKMLFLPDSISEMFLFQSLFPLATVYLVYSHLKEYAVSWFS	54	
QY	563	LVIGMLNLVYTRNGFOHTGIYSVMIQVYLIDRLFRLLVLYVLFGEFAVALVSLSQEA--	62	
Db	545	LALGNTNMLLYTRFGQMGIVAVIAWIEKMILLDLCRFMEYVIVLFGRSTAVVLEIDGKN	60	
QY	621	WREATAFGPAATSVQPMESQDEBNGAQYRGILGSLSELFKTTIMGE	66	
Db	605	DLSPESTSHRRWRPAPCRPDS-----YNSLYSTCLELFTKTTIMGD	64	
QY	670	LAFQOLHFQGMVLLLLAVLYLLIILLNMLIALMSEYNSVATDSMSIMKLOKAISVL	72	
Db	648	LEFENUDFNKAVFILLLAYVILYIILLNMLIALMSEYNTKINQESKNIMKLOKATITIL	70	
QY	730	EMENGYMWC-RKKQDAQVMLTVGTRPGSGPDERKCFVNEYEYNWASWEGQLPTLCEDPSGA	78	
Db	708	DTEKSFSLCKMKHKKERSKLLQVGTGPKGDKDYRWCFVDEVMNTVNTNGIINEDPGNC	76	
QY	789	GVPRTELENPLVASPPKDEDEGASAEENYVYPOLLQ 822		
Db	768	EGVKRTLSFSLRSS----RVSGRMKMKFALVPLLR 798		

RESULT	7
09H304	
ID	09H304
AC	PRELIMINARY
DT	01-MAR-2001 (TREMblrel. 16, Created)
DT	01-MAR-2001 (TREMblrel. 16, Last sequence update)
DT	01-MAR-2001 (TREMblrel. 16, Last annotation update)
DE	CAPSNA1CN RECEPTOR.

01-MAR-2001 (TREMblrel. 15, last annotation update)
DE HYPOTHETICAL 94.9 KDA PROTEIN.
GN DKFZP434K0220.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=TESTIS;
RA Ottenwaelder B., Obermaier B., Mewes H.W., Gassenhuber J., Wiemann S.;
RL Submitted (JAN-2000) to the EMBL/Genbank/DBJ databases.
DR EMBL: AL136801; CAB66735.1; -
KW Hypothetical protein.
SQ SEQUENCE 839 AA; 94950 MW; EA9BF7D603AE4760 CRC64;

Query Match 37.1%; Score 1625.5; DB 4; Length 839;
Best Local Similarity 48.8%; Pred. No. 2,3e-116;
Matches 339; Conservative 118; Mismatches 193; Indels 45; Gaps 11;

149 EDLAGLPEYLSTSKYLTDESEYEGSTGKTCMKAVLNKDGVCNACILPLQIDRDGPN 208
128 QDLESLLFLQSKKHLDNEFKDPETGKTCCKLKMNLNHDQNTTIPLEIAQTDSL 187
209 QPLVNAOCTDDYYRGHSALHIAIEKRSLOCVKLVENGANVHARACGREFOKGOG-TCFY 267
188 KELVNASYTDSSYKGGTALHIAIERNNMALTYLLVENGADVOAAAHGDFEKKTKRPGFY 247
268 FGEPLSLAAGCKOMDVSYLLENPHOPASLOATSOQNTVHALVMISDNNAENALVT 327
248 FGEPLSLAAGCKOMDVSYLLENPHOPASLOATSOQNTVHALVMISDNNAENALVT 307
328 SMYDGLLOAGARLCTPVQLEDIRNODLPLKLAKKEGIEIFRHILQREFS--GLSHLS 385
308 SKYNELILIGAKLHTLTKLEELTNKKGMPTLALAGTGKIGVLAITLOEIOEPERCHLS 367
386 RKFTWCYGPVAVSLYDLASVDSCEENSVLEIIAF-HCKSPRRHNVVLEPINKLLQAKW 444
368 RKFTWAGPVHVSXYDLSCIDTCENSVLEVIAYSSSETPRRHMLLVEPLNRLLODKW 427
445 DLLIRK-FFLNPLCLNLYFTFAVAYHOPITLKAAPLKA-E-VGNSMLLGHILLIG 502
428 DREVKRIFFNPLVCLNLYFTFAVAYHOPITLKAAPLKA-E-VGNSMLLGHILLIG 484
503 GYLLVGOALMYFRRHVFIMISIDSYFEILFQALLTVVSQVCFLAIEVYPLDLYSA 562
485 GYVFFFRGQYGLQRRSPSKITLFVDSYSEMLFFLOSFLATVLYLFSLKRYVASMVS 544
563 LVYGLNLLYYTRGFQHTGYSVMIOKYLRLDLRLFLLYLVLFGLFAVALVLSQEA-- 620
545 LALGWTNMLYYTRGFQHTGYSVMIOKYLRLDLRLFLLYLVLFGLFAVALVLTLEDGKN 604
621 -----WRPEAPPGPNATESVQPMESGDEGNGAQYIGILASLELKFPTIGKE 669
605 DSLPSSSTSHRRKRGPCRPDSS-----YNSLSTCELEKFTIGMD 647
670 LAFEOELRGWVLLLLAYVLLTYTLLMLTALMSETSVANTDSIMKLOKAIISVL 729
648 LEFTEYDPAKAFIILLAYVLLTYTLLMLTALMSETSVANTDSIMKLOKAIISVL 707
730 EMEGNYMWC-RKKORAGVMLTYGTPDSDPERMCPREVEVWMAWMEOTLPLCEDPSGA 788
708 DEKESLTKMKRAFRSGKILQGYTPDGDYRMCFRVDEVMYMTWMTVGIINEDPGNC 767
789 -GVPTLENPLVLAPEKDEGASSENYVPVOLLQ 822
768 EGVKRTLSFSLKSS-----RVSGRHKMKNFALVPLLR 798

09NOV74:
01-OCT-2000 (TREMblrel. 15, Created)
01-OCT-2000 (TREMblrel. 15, last sequence update)
01-MAR-2001 (TREMblrel. 15, last annotation update)
DE VANILLOID RECEPTOR 1.
GN VRL
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Kelsell R.E.;
RL Submitted (Apr-2000) to the EMBL/Genbank/DBJ databases.
[2]
SEQUENCE FROM N.A.
RA Hayes P., Meadows H.J., Harries M.H., Duckworth M.D., Cairns W.,
RA Harrison D.C., Clarke C., Gunthorpe M., Ellington K., Pirinjah R.K.,
RA Barton A.J., Medhurst A.D., Smith G.D., Topp S., Mordock P.,
RA Sanger G.D., Terrett J., Jenkins O., Randall A., Benham C.D.,
RA Gloger I.S., Davis J.B.;
RT "Cloning and functional expression of a human orthologue of rat
vanilloid receptor-1";
RL Submitted (JUN-2000) to the EMBL/Genbank/DBJ databases.
DR EMBL: AJ277028; CAB95729.1; -
DR InterPro: IPR002110; -
DR InterPro: IPR002111; -
DR Pfam: PF00023; ank; 3.
DR PROSITE: PS50088; ANK_REPEAT; 1.
DR PROSITE: PS50297; ANK_REPEAT_REGION; 1.
DR SMART: SM00248; ANK; 1.
KW Receptor.
SQ SEQUENCE 839 AA; 94923 MW; 7142FEAE43189ECC CRC64;

Query Match 37.1%; Score 1621.5; DB 4; Length 839;
Best Local Similarity 48.8%; Pred. No. 4.7e-116;
Matches 339; Conservative 117; Mismatches 194; Indels 45; Gaps 11;

149 EDLAGLPEYLSTSKYLTDESEYEGSTGKTCMKAVLNKDGVCNACILPLQIDRDGPN 208
128 QDLESLLFLQSKKHLDNEFKDPETGKTCCKLKMNLNHDQNTTIPLEIAQTDSL 187
209 QPLVNAOCTDDYYRGHSALHIAIEKRSLOCVKLVENGANVHARACGREFOKGOG-TCFY 267
188 KELVNASYTDSSYKGGTALHIAIERNNMALTYLLVENGADVOAAAHGDFEKKTKRPGFY 247
268 FGEPLSLAAGCKOMDVSYLLENPHOPASLOATSOQNTVHALVMISDNNAENALVT 327
248 FGEPLSLAAGCKOMDVSYLLENPHOPASLOATSOQNTVHALVMISDNNAENALVT 307
328 SMYDGLLOAGARLCTPVQLEDIRNODLPLKLAKKEGIEIFRHILQREFS--GLSHLS 385
308 SKYNELILIGAKLHTLTKLEELTNKKGMPTLALAGTGKIGVLAITLOEIOEPERCHLS 367
386 RKFTWCYGPVAVSLYDLASVDSCEENSVLEIIAF-HCKSPRRHNVVLEPINKLLQAKW 444
368 RKFTWAGPVHVSXYDLSCIDTCENSVLEVIAYSSSETPRRHMLLVEPLNRLLODKW 427
445 DLLIRK-FFLNPLCLNLYFTFAVAYHOPITLKAAPLKA-E-VGNSMLLGHILLIG 502
428 DREVKRIFFNPLVCLNLYFTFAVAYHOPITLKAAPLKA-E-VGNSMLLGHILLIG 484
503 GYLLVGOALMYFRRHVFIMISIDSYFEILFQALLTVVSQVCFLAIEVYPLDLYSA 562
485 GYVFFFRGQYGLQRRSPSKITLFVDSYSEMLFFLOSFLATVLYLFSLKRYVASMVS 544
563 LVYGLNLLYYTRGFQHTGYSVMIOKYLRLDLRLFLLYLVLFGLFAVALVLSQEA-- 620
545 LALGWTNMLYYTRGFQHTGYSVMIOKYLRLDLRLFLLYLVLFGLFAVALVLTLEDGKN 604
621 -----WRPEAPPGPNATESVQPMESGDEGNGAQYIGILASLELKFPTIGKE 669

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Db 605 DSLPESESTSHRMGRPACRPDSS-----YNSLXSTCLEFKFTTGMGD 647
QY 670 LAPQDQHFQGVLLLLAYVLLTYILLNMLIMSETVNSVATDSIMWLKRAISVL 729
Db 648 LEFTENQDFKAVFIILLAYVLLTYILLNMLIMSETVNSVATDSIMWLKRAISVL 707
QY 730 EMENGYMWC-RKKORAGVMLTVGKPPDGSPPDERKCFRVEEYNASMEQTLPTLCEDEPSGA 788
Db 708 DTEKSPFKCKRKAFFRSKLLQVGYTPDGKDDYKRCFDEYVNTMTNNGIINDEPGNC 767
QY 789 -GVPTLENPLVASPPKEDDGASEENVYVOLLQ 822
Db 768 EGVKRTLSFSLRSS-----RVSGRHMKNFALVPLLR 798

RESULT 10
ID 035433 PRELIMINARY; PRT: 838 AA.
AC 035433;
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE VANILLOID RECEPTOR SUBTYPE 1.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98007969; PubMed=9349813;
RA Carlier M.J., Schumacher M.A., Tomlinaga M., Rosen T.A., Levine J.D.,
RA Julius D.;
RT "The capsaicin receptor: a heat-activated ion channel in the pain
RT pathway.";
RL Nature 389:816-824(1997).
DR EMBL: AF029310; AAC53398.1;
DR InterPro: IPR002110;
DR InterPro: IPR002111;
DR Pfam: PF00023; ank; 3.
DR PROSITE: PS50088; ANK_REPEAT; 1.
DR PROSITE: PS50297; ANK_REP_REGION; 1.
DR SMART: SM00248; ANK; 1.
SQ SEQUENCE 838 AA; 94947 MW; DAFCC80B12BD71BF CRC64;

Query Match 37.0%; Score 1618; DB 11; Length 838;
Best Local Similarity 43.1%; Pred. No. 8.7e-116;
Matches 360; Conservative 128; Mismatches 228; Indels 120; Gaps 17;

QY 18 GOEDSEADRGKLDGSGLPPEMSQFQGEDRKFAPOIRVN---LNYRKGTG----- 65
Db 51 GKGDSEAS-----PLDCPYEEGGLASCPITVSSVLTIRPDGDPASVAPSSQ 99
QY 66 ---ASQDPNFRDRLFNNAVSRGVPGAGATCGGCTGCAGACTTCAGAGACTGAGC 121
Db 100 DSVSAGEKPPRLYDRSRJFDVAQAQ----- 123
QY 122 AAGACCAGCACTGACGACGCTGEDIAGLPPELSTSKYLNDSVETGEGTGCTCM 181
Db 124 -----SNC-----QELSELPLFLOKSKRLTDSERKDEGTGCTCL 159
QY 162 KAVLNKQGVNACILPLLIQIDRSGNPOPLVNAOCTDDYRGSHALHIEKRSLOCYKL 241
Db 160 KAVLNKQGVNACILPLLIQIDRSGNPOPLVNAOCTDDYRGSHALHIEKRSLOCYKL 219
QY 242 LVENGANHAACGFFQKGG-TCFYFGEPLSLAACKQMDVSYLIENPHQASLOA 300
Db 220 LVENGANHAACGFFQKGG-TCFYFGEPLSLAACKQMDVSYLIENPHQASLOA 279
QY 301 TDSQGNVYLAHLYMDSAEENIALVTSMYDGLQAGARICCTVLEDIRNQLDTPLKL 360
Db 280 RDSVGNVYLAHLYMDSAEENIALVTSMYDGLQAGARICCTVLEDIRNQLDTPLKL 339

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QY 361 AAKGKIEIFRHLQREF--SGLSLRKKEFWCYGPRVSLYDLASVCEENSYLEII 418
Db 340 AASGKIGVLAIVLQRIHEPECHLSRKTEWAGYVSHSLYDSCIDCEKNSYLEVI 399
QY 419 AF-HCKSPHRRMYVLEPLKLLQAKMDLTPK-FELNLCNLIMYFIFVAVAHQPTLK 476
Db 400 AYSSSETPNRRHMLVPLNLLQDKMDRFVKRIEFENFVYCYMIIFLAAYRYRV-- 457
QY 477 KOAAP--HLKAEVNSMLTGHLIILGGLYLLVGLMYFRNRVFWISFIDSEILF 534
Db 458 -EGLPFKLNTVGDYRVRVGEILLVSGGVYFEFRGQYFLQRRPSLKSLEVSYSILF 516
QY 535 LFOALLTVSQCFLFAIEWYLPPLVSLVGLNLTLYTRGFOHTIYSVMIQKVL 594
Db 517 FVQSLFMYLVSVLYEFSGRKEVASMVSFLAMGNTMLYTRGQOMGIYAVMIKMLRD 576
QY 595 LIRFLIYLVFLGFAVALVLSQEAHPAPGPNNTESVOPMEGDEGNGA----- 648
Db 577 LCRFMFYLVFLGFSYAVVTLIED-----GKN---NSLPWESYPHKCRSACKPN 625
QY 649 QYRGILLASLELFFETTGMEGLAFQDQHFQGVLLLLAYVLLTYILLNMLIMSET 708
Db 626 SYNSLSTCLELRFETIGMDLEFTEYDFAVFIILLAYVLLTYILLNMLIMSET 685
QY 709 VNSVATDSIMWLKRAISVLEMEGMYWC-RKKORAGVMLTVGTPDGSPPDERKCFRVE 767
Db 686 VNKIAQESKNIMKLRATITLIDREKSLCKMKRAFPKSGKLLQVGFPPDGDDYKRCFDE 745
QY 768 EVNMAWSEQTLPTLCEDEPSGA-GVPTLENPLVASPPKEDDGASEENVYVOLLQ 822
Db 746 EVNMTWTNVTNNGIINDEPGNCEGVKRTLSFSLRSS-----RVSGRHMKNFALVPLLR 797

RESULT 11
ID 09JMS7 PRELIMINARY; PRT: 838 AA.
AC 09JMS7;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE VANILLOID RECEPTOR TYPE 1 LIKE PROTEIN 1.
GN VR1L1.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RA Tsutsuni S., Nakamura A., Kohama K.;
RT "Vanilloid receptor type 1 like protein 1.";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AB040873; BA94307.1;
DR InterPro: IPR002110;
DR InterPro: IPR002111;
DR Pfam: PF00023; ank; 3.
DR PROSITE: PS50088; ANK_REPEAT; 1.
DR PROSITE: PS50297; ANK_REP_REGION; 1.
DR SMART: SM00248; ANK; 1.
DR KW Receptor.
SQ SEQUENCE 838 AA; 94964 MW; EE33CE4A606C3404 CRC64;

Query Match 37.0%; Score 1618; DB 11; Length 838;
Best Local Similarity 43.1%; Pred. No. 8.7e-116;
Matches 360; Conservative 128; Mismatches 228; Indels 120; Gaps 17;

QY 18 GOEDSEADRGKLDGSGLPPEMSQFQGEDRKFAPOIRVN---LNYRKGTG----- 65
Db 51 GKGDSEAS-----PLDCPYEEGGLASCPITVSSVLTIRPDGDPASVAPSSQ 99
QY 66 ---ASQDPNFRDRLFNNAVSRGVPGAGATCGGCTGCAGACTTCAGAGACTGAGC 121
Db 100 DSVSAGEKPPRLYDRSRJFDVAQAQ----- 123

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OC Mammalia; Euthera; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=RENAL CORTEX;
 RX PubMed=11025659;
 RA Strömman R., Harteneck C., Nunnemacher K., Schultz G., Plant T.D.;
 RT "OTRPC4, a nonselective cation channel that confers sensitivity to
 extracellular osmolarity";
 RL Nat. Cell Biol. 2:695-702(2000).
 DR EMBL: AF58465; AAC616127.1;
 SQ SEQUENCE 871 AA; 98294 MW; C62056B86DEA6FB6 CRC64;

Query Match 32.7%; Score 1430; DB 4; Length 871;
 Best Local Similarity 40.3%; Pred. No. 2.5e-101;
 Matches 341; Conservative 114; Mismatches 244; Indels 148; Gaps 18;

OY 8 PVFRLTLDDGGQEDG-----SEADRGK-LDFGSGLPMEGSGQEDGRKAP----- 52
 DB 32 PLSSLANLFEFG-EDGSLSPPADSRAPGPDGRPNLRMKFGAFRGVNPIDLESTL 90
 OY 53 -----QIRVNLNRYK-----GTGASQPD--NRFD 75
 DB 91 YESSVYGPKKAPMDSLFDYGYRHHSSDMKRMKRIIEKQPSKAPAPQPPILKAVN 150
 OY 76 RDLFNANVSAGVAGAGATGCTGCTGAGACTCCAGACTACCTGAGCAAGACCAAGTA 135
 DB 151 RPILEDIVSRG-----STA 164
 OY 136 CCTCACCAGACTCGEDLAGLPEVLSKTSKYLTDSEYTESGTCTCLMAVNLKQGVNACI 195
 DB 165 -----DLDGLSLTLTHKKRLTDEFEFREPSTGKTCLPKALLNLSNGRNDTI 210
 OY 196 LPLQIDRDSGNPOPLVNAOCTDDYRGHSALHAIERKSLQCVKLIVNGANVHARAG 255
 DB 211 PVLDDIAERTGNMREFINPFDIYRGOTAHAIERCKHYVELVAOGADVHAQARG 270
 OY 256 RFQO-KGGGTCTFFGELPLSLAACKTQMDVSYLLENPHQASLOATDSQNTVLHALVM 314
 DB 271 REFQPDDEGGYFEGELPLSLAACKTQMDVSYLLENPHQASLOATDSQNTVLHALVM 330
 OY 315 ISDNSAENIALYTSWYDGLLOAGARLCPVOLEDIRNLODLPFLAKAEGKIEIFRHIL 374
 DB 331 IADNRENTKFTKMYDILLKCARLPDSNLETYVLANNGLSPLMAAKTGKIGVFOHII 390
 OY 375 QREFS--GLSHLSRKFTTECYGPRVRSYLDLASVDS--EENSYLEIIAFHCKSPRHRY 431
 DB 391 RREYVDEDETRHLSRKFKMAVGPVYSLSLDSLTGCEBASVLELIVNSKIENRHEML 450
 OY 432 VLEPLNKLLOAKMDLL-IPKFFLNFLCNLIYFIFTAVAYHQPFLKQAPHLKAEVNS 490
 DB 451 AVEPINELLRDKMRKFGAVSFYINVSYLCAVYIFTLAYYQPL--EGRPPIYRTTYDV 508
 OY 491 MLTGHILLIGGIVLLVQGLM-YFRRHNVFTWISTDYSEFELFELFOALLTVVSOVLCE 549
 DB 509 LTLAEVITLFTGVLFPTTINIDLMFKKCPGVNSLFDISGFOLLYFISVLIVSAALYL 568
 OY 550 LAIEWYLPPLVSAVLVGLNLLYTRGFOHTGYSVMIOKVLIRDLRLLYIVLRF 609
 DB 569 AGIEAYLVAVVAVLVGLNLLYTRGFOHTGYSVMIOKVLIRDLRLLYIVLRF 628
 OY 610 AVALVSL-----SOEAMRPAEPGPNNTESVQPMGEDEGNGAQQVIGILEASLE 659
 DB 639 ASALVSLNIPCANMKVCEVDQNTCTVPTVPCRS-----ETFTFL--LD 672
 OY 660 LKFTIGGELAFQQLHPRGVALLLLAYVLTITLLNMLIALMSEVNSVANDSNTI 719
 DB 673 LKFTIGGELAFQQLHPRGVALLLLAYVLTITLLNMLIALMSEVNSVANDSNTI 732
 OY 720 WKLOKRAISVLEWENGY-WMCRKQKQAGVNLVGTGPDSPDRRCFVYEVVWMAWQDTL 778
 DB 733 WKLOKRAISVLEWENGY-WMCRKQKQAGVNLVGTGPDSPDRRCFVYEVVWMAWQDTL 792

OY 779 PLYCEDP 785
 DB 793 GIINEDP 799

RESULT 14
 OYER28 PRELIMINARY; PRT: 871 AA.
 AC OYER28:
 DT 01-MAR-2001 (TREMblrel. 16, Created)
 DT 01-MAR-2001 (TREMblrel. 16, Last sequence update)
 DT 01-MAR-2001 (TREMblrel. 16, Last annotation update)
 DE VANILLOID RECEPTOR-RELATED OSMOTICALLY ACTIVATED CHANNEL.
 GN VROAC.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=KIDNEY;
 RX PubMed=11081638;
 RA Liedtke W.B., Choe Y., Marti-Renom M.A., Bell A.M., Denis C.S.,
 RA Sall A., Hudspeth A.J., Friedman J.M., Heller S.;
 RT "Vanilloid receptor-related osmotically activated channel (VR-ORC), a
 candidate vertebrate osmoreceptor";
 RL Cell 103:525-535(2000).
 DR EMBL: AF263521; AAG28027.1;
 KW Receptor.
 SQ SEQUENCE 871 AA; 98009 MW; 5D50684DA08C354B CRC64;

Query Match 32.6%; Score 1428.5; DB 11; Length 871;
 Best Local Similarity 37.9%; Pred. No. 3.3e-101;
 Matches 343; Conservative 128; Mismatches 255; Indels 179; Gaps 18;

OY 8 PVFRLTLDDGGQEDG-----EADRGK-LDFGSGLPMEGSGQEDGRKAP----- 52
 DB 32 PLSSLANLFEFGSSSLSPVDSR--PAGEGDRPNLRMKFGAFRGVNPIDLESTL 90
 OY 53 -----QIRVNLNRYKGTGASQPDPNR-----FD 75
 DB 91 YESSVYGPKKAPMDSLFDYGYRHHSPDMKRMKRVVEKQPSKAPAPQPPILKAVN 150
 OY 76 RDLFNANVSAGVAGAGATGCTGCTGAGACTCCAGACTACCTGAGCAAGACCAAGTA 135
 DB 151 RPILEDIVSRG-----STA 164
 OY 136 CCTCACCAGACTCGEDLAGLPEVLSKTSKYLTDSEYTESGTCTCLMAVNLKQGVNACI 195
 DB 165 -----DLDGLSLTLTHKKRLTDEFEFREPSTGKTCLPKALLNLSNGRNDTI 210
 OY 196 LPLQIDRDSGNPOPLVNAOCTDDYRGHSALHAIERKSLQCVKLIVNGANVHARAG 255
 DB 211 PVLDDIAERTGNMREFINPFDIYRGOTAHAIERCKHYVELVAOGADVHAQARG 270
 OY 256 RFQO-KGGGTCTFFGELPLSLAACKTQMDVSYLLENPHQASLOATDSQNTVLHALVM 314
 DB 271 REFQPDDEGGYFEGELPLSLAACKTQMDVSYLLENPHQASLOATDSQNTVLHALVM 330
 OY 315 ISDNSAENIALYTSWYDGLLOAGARLCPVOLEDIRNLODLPFLAKAEGKIEIFRHIL 374
 DB 331 IADNRENTKFTKMYDILLKCARLPDSNLETYVLANNGLSPLMAAKTGKIGVFOHII 390
 OY 375 QREFS--GLSHLSRKFTTECYGPRVRSYLDLASVDS--EENSYLEIIAFHCKSPRHRY 431
 DB 391 RREYVDEDETRHLSRKFKMAVGPVYSLSLDSLTGCEBASVLELIVNSKIENRHEML 450
 OY 432 VLEPLNKLLOAKMDLL-IPKFFLNFLCNLIYFIFTAVAYHQPFLKQAPHLKAEVNS 490
 DB 451 AVEPINELLRDKMRKFGAVSFYINVSYLCAVYIFTLAYYQPL--EGRPPIYRTTYDV 508

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: October 4, 2001, 08:18:30 ; Search time 1846.36 Seconds
(without alignments)
12640.598 Million cell updates/sec

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Gapop 60.0 , Gapext 60.0

Searched: 10228115 segs, 4726426750 residues

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Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

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252: gb_estf83:*
253: gb_estf84:*
254: gb_estf85:*
255: gb_estf86:*
256: gb_estf87:*
257: gb_estf88:*
258: gb_estf89:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.


```

RESULT 2
LOCUS BP940288/c 588 bp mRNA EST 22-JAN-2001
DEFINITION 7043106.x1 NCI-CGAP_Kid1 Homo sapiens cDNA clone IMAGE:3577090 3'
            similar to TR:09Y5S1 09Y5S1 VANILLOID RECEPTOR-LIKE PROTEIN 1.1;
            mRNA sequence.
ACCESSION BP940288
VERSION BP940288.1 GI:12357608
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
            Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 588)
            NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
            National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
            Unpublished (1997)
JOURNAL Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-remail.nih.gov
            Tissue Procurement: Christopher Koskaluk, M.D., Ph.D., Michael R.
            Emmert-Buck, M.D., Ph.D.
            CDNA Library Preparation: M. Bento Soares, Ph.D.
            DNA Sequencing by: Washington University Genome Sequencing Center
            Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNT, send email to:
            inf@image.llnl.gov
            Seq primer: -40UP from gibco
            High quality sequence stop: 492.
FEATURES
    source
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            /organism="Homo sapiens"
            /db_xref="taxon:9606"
            /clone="IMAGE:3577090"
            /clone_1lb="NCI-CGAP_Kid1"
            /lab_host="DH10B"
            /note="Organ: Kidney; Vector: pT73D-Pac (Pharmacia) with
            a modified polylinker; Site_1: Not I; Site_2: Eco RI;
            Plasmid DNA from the normalized library NCI-CGAP_Kid1 was
            prepared, and ss circles were made in vitro. Following HAP
            purification, this DNA was used as tracer in a subtractive
            hybridization reaction. The driver was PCR-amplified cDNAs
            from a pool of 5,000 clones made from the same library
            (clones 132276-132391, 145607-145675, and
            150552-150285). Subtraction by Bento Soares and M.
            Fatima Bonaldo."
BASE COUNT 110 a 173 c 163 g 142 t
ORIGIN
Query Match 23.8%; Score 588; DB 171; Length 588;
Best Local Similarity 100.0%; Pred. No. 1.3e-288;
Matches 588; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 97 atgacctaccctccagctccagtttcagtttgaggaacattgatgagagcccaaga 156
DB 588 ATGACCTACCCCTCCAGCTCTCCAGTTTCAGGTGGAGACATTAGATGAGGCCAAGAA 529
QY 157 gatggtctgtaggagcgagagaaagctgattttgtagcgagcggtccctccatgag 216
DB 528 GATGGCTCTGAGGCGGACAGAGAAAGCTGGATTTGGAGGCGGTCTGCTCCATGAG 469
QY 217 tcaacgttccagggcgagagacccgaattccgacctcagataagatcaactcaactac 276
DB 468 TCACACTTCACAGGCGGACGAGAAATTCGCCCTCAAGATTAAGAGTCAACCTCAACTCA 409
QY 277 cgaagaaggagaggtgacagctcagcgagatccaacccagtttgacccagatggtcttc 336
DB 408 CCAAAAGGAAAGGTGCTCCAGTACGCCGATTCAAAACCGATTGACCGAATGCGCTCTTC 349
QY 337 aatgggtctcccggtgtgtcccgagagatctgctggaactccagagtaactgagcaag 396

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DB 348 AATCGGCTCTCCGGGGGTGTCGCCGAGATCTGGCTGACTTCCAGACTCAGCCAG 289
QY 397 accagaagctacatcaacgagctcggaatcacagaagggtccacaggttaagagctg 456
DB 288 ACCAGCAAGTACTCCTACCGACTCGGATATCACAGAGGCTCCACAGGTAAGACTGCTG 229
QY 457 atgaaggctgtgtgaaccttaaggaagagatgaatgcctgcatcttcgacctgtcag 516
DB 228 ATGAAGGCTGTGCTGAACCTTAAGGAGGAGTCAATGCTGCAATTCGACACTGCTCAG 169
QY 517 atggaagagagctctggaacctctcagccccctgtaaatgccaagtcacagatgactat 576
DB 168 ATGAGAGGAGACTCTGGCAATCTCAGCCCTGTAATGCCAGTCCACAGATGACTAT 109
QY 577 taccagagccagagcgctctgacacatcgccattgaagaagagaggttcgagtgtaag 636
DB 108 TACCGAGGCCACAGCCCTCTGCACATCGCATTTGAGAGAGAGACTGTGCAGTGTGAAG 49
QY 637 ctccctgtgtagaagtgggccaatgtgcatgcccggcctgcgagcgc 684
DB 48 CTCCTGTGTGAGAAATGGGCGCAATGTGCATGCCCGGCGCTGCGCGCGC 1
RESULT 3
LOCUS AM976725/c 686 bp mRNA EST 02-JUN-2000
DEFINITION EST388834 MAGE resequences, MAGO Homo sapiens cDNA, mRNA sequence.
ACCESSION AM976725
VERSION AM976725.1 GI:8167958
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
            Chordata; Craniata; Vertebrata; Euteleostomi;
            Eukaryota; Metazoa; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 686)
            Hegde, P., Qi, R., Abernathy, K., Dharp, S., Gaspard, R., Gay, C., Holt
            , I.E., Saeed, A.I., Sharov, V., Lee, N.H., Yeatman, T.J. and
            Quackenbush, J.
            Assessment of gene expression patterns in a model of colon tumor
            metastasis using a 19,200 element cDNA microarray
            Unpublished (2000)
JOURNAL Contact: John Quackenbush
            The Institute for Genomic Research
            9712 Medical Center Dr., Rockville, MD 20850, USA
            Tel: 301 838 3528
            Fax: 301 838 0208
            Email: john@tigr.org
            Plate: 364
            Seq primer: Forward.
FEATURES
    source
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            /organism="Homo sapiens"
            /db_xref="taxon:9606"
            /clone_1lb="MAGE resequences, MAGO"
            /note="Vector: pBluescriptSm"
BASE COUNT 124 a 195 c 199 g 168 t
ORIGIN
Query Match 22.6%; Score 559; DB 123; Length 686;
Best Local Similarity 100.0%; Pred. No. 8.2e-274;
Matches 559; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 126 caggttggagacattagatgagagcgaagaatgctctgagggcgagagaggaagct 185
DB 565 CAGGTTGGAGACATTAGATGAGAGGCCAAGAATGCTGTGAGCGGACAGAGAAAGCT 506
QY 186 ggaatttggagcggtgtgctcccatggaagtcacagttccagggcgagagcgaat 245
DB 505 GGATTTGGAGACGGGCTCCTCCATGAGTACAGTTCACAGGGGAGAGACCGGAAT 446
QY 246 gggccctgataaagatcaactcaactcgaagaaggaaagtgccagtcagcgga 305

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Db 445 GGGCCCTCAGATAGACGACCTCACTACCGAAGGGAACAGTGGCCAGTCAGCCGGA 386
 Qy 306 tccaaaccgatttaccgagatcggctcttcaatgagtgctcccgagggtgctcccgaggga 365
 Db 385 TCCAAACCGATTGACGAGATCGGCTCTTCAATCGGCTCTCCCGGGGTGTCGCCGAGGA 326
 Qy 366 tcttgctggagatttccagatgctcctgagagaagaacagcaagtaactaccgaactcggaata 425
 Db 325 TCTGGCTGGAGATTCCAGATGCTGAGACAAAGCAGCAAGTACCTCAGCTCGGAATA 266
 Qy 426 cacagagggctcccaagagtaagacgtgctgatgaagagctgtgctgaagccttaagaagag 485
 Db 265 CACGAGAGGCTCCACAGATGAGAGCTGCTGCTATGAGAGCTGTGCTGACCTTTAAGAGAGG 206
 Qy 486 agtaatgctgcatcttgcacatgctgctgagatcgacagagagctctggcaatcctcagcc 545
 Db 205 AGTCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 146
 Qy 546 cctggttaagctccagagcaagatgacatattaccgagagcagcagcgtctgacatcgc 605
 Db 145 CCTGCTAAATGCTCCAGTGCACAGATGACTATTACCGAGGCCACAGCCTCTGCAATCGC 86
 Qy 606 cattgagaagagagctgctgagctgtgtgaagctcctggtgagagatgaggcgaatgtgca 665
 Db 85 CATTGAGAAAGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 26
 Qy 666 tggccgggctgctgagcgc 684
 Db 25 TGCCCGGGCTGGCGGCCG 7
 RESULT 4
 BG254423 953 bp mRNA EST 13-FEB-2001
 LOCUS 602369021F1 NIH_MGC_91 Homo sapiens cDNA clone IMAGE:4477157 5',
 DEFINITION mRNA sequence.
 ACCESSION BG254423
 VERSION BG254423.1 GI:12764239
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 REFERENCE 1 (bases 1 to 953)
 NIH-MGC http://mgi.nci.nih.gov/.
 AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cga@bbs-remail.nih.gov
 Tissue Procurement: DCTD/DRP
 CDNA Library Preparation: Life Technologies, Inc.
 DNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
 http://image.llnl.gov
 plate: L1AM10305 row: j column: 06
 High quality sequence stop: 676.
 Location/Qualifiers
 1..953
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:4477157"
 /clone_1lb="NIH_MGC_91"
 /tissue_type="adenocarcinoma, cell line"
 /lab_host="DH10B (phage-resistant)"
 /note="Organ: prostate; Vector: pCMV-Sport6; Site_1: NotI;
 Site_2: SalI; Cloned unidirectionally; oligo-dT primed.
 Average insert size 1.4 kb. Library enriched for
 full-length clones and constructed by Life Technologies.
 Note: this is a NIH_MGC Library."
 BASE COUNT 201 a 284 c 269 g 199 t
 ORIGIN

Query Match 21.7%; Score 536; DB 175; Length 953;
 Best Local Similarity 99.8%; Pred. No. 4.6e-262;
 Matches 586; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 627 gctgtgaagctcctggtgagaaatgaggaatgcatgcatgcccggcctgagcctt 686
 Db 41 GGTGTGTAAGCTCCGTGGTGGAGAAATGGGCAATGTGATGATCCCGGGCTCGGCGCTT 100
 Qy 687 ctccagaagggccaaaggaactgtcttattcctggtgagatgacctctcttggccgc 746
 Db 101 CTTCCAGAGGGCCCAAGGAGCTTGTATTGTTGAGTACCTCCCTCTTGTGGCGC 160
 Qy 747 ttgcaaccaagagtgagatgtgtgtaagctactcctgtgagaaaccaacagcccgccag 806
 Db 161 TTGCACCAAGCAGTGGATGTGTGTAAGTACTCTCTGAGAAACCAACAGCCGCGCAG 220
 Qy 807 cctgcaagggcactgactccagaggaacacagctcctgcatgcccctagtgatcctgga 866
 Db 221 CCTGACAGGCCACTGACTGCTCCAGGGCAACAGTCTCTGATGCCCTAGTATGATCTGGA 280
 Qy 867 caactcagctgagaaacattgcactgtgtgacagcagcatgatagtggtcctccaagcttg 926
 Db 281 CAACTCAGCTGAGAACTTGCATGTGTGACCCAGCATGATGATGAGCTCCCTCCAAGCTGG 340
 Qy 927 gggccgctctgacctaccgctgagctgagatcctgcaactgagatgagatcctcaagcc 986
 Db 341 GGGCCGCTCTGCTCTACCTGACGCTTGAGAGACATCCGCAACTGAGAGATCCACAGCC 400
 Qy 987 tctgaagctgcccagcaagagaggaagatcgagatttccagacacatcctcagcagcagga 1046
 Db 401 TCTGAAGCTGGCCGCCAAGAGAGGGCAAGATCGAATTTTCAAGCAGATCTCCAGCGGGA 460
 Qy 1047 gtttcaagctgagcagcacttcccgaaagtccagagtggtgctatgagcctgtcgcg 1106
 Db 461 GTTTTCAGGAGCTGAGCCACTTCCCGAAAGTTCACGAGAGGTGATGAGGCTGTCGC 520
 Qy 1107 ggtgtgctgtatgactgctctgtgagacagctgtgagaggaacacagctgtctgagat 1166
 Db 521 GGTGTGCTGTATGACTGCTGCTGTGTGACCGCTGTGAGAGAAACCAATGTCTGAGAT 580
 Qy 1167 catgcttccatgcaagagccgcagcagcagcagcagcagcagcagcagcagcagcagc 1213
 Db 581 CATTGCTTTTATTCAGAAAGCCCGGACCCAGACCAAGATGCTCTTT 627
 RESULT 5
 BF436096 513 bp mRNA EST 30-MAR-2001
 LOCUS nab77a02.x1 Soares_NSF_FB_9W_OT_PA_P-S1 Homo sapiens cDNA clone
 DEFINITION IMAGE:3273507 3', similar to TR:09Y5S1 Q9Y5S1 VAVILLOID
 RECEPTOR-LIKE PROTEIN 1.; contains Alu repetitive element.; mRNA
 sequence.
 ACCESSION BF436096
 VERSION BF436096.1 GI:11448411
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 REFERENCE 1 (bases 1 to 513)
 NCI-CCGAP http://www.ncbi.nlm.nih.gov/ncicgap.
 Tumor Gene Index
 Unpublished (1997)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cga@bbs-remail.nih.gov
 This clone is available royalty-free through LNL; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.
 Seq primer: -40UP from Gibco
 High quality sequence stop: 423.
 Location/Qualifiers
 FEATURES

source 1. 513

/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3273507"
/lab_host="DH10B"
/note="Organ: pooled; Vector: pRT3D-Pac (Pharmacia) with a modified polylinker; Site: 1: Not I; Site: 2: Eco RI; Equal amounts of plasmid DNA from five normalized libraries were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 5 libraries. The pools consisted of the following libraries and clones: Soares NBHSF pool 1: 309384-310919, 323208-325895 Soares NB2HP pool 1: 145032-147335, 147720-148103, 148872-149255, 15002 - 150407, 151176-152327 Soares NB2HF8-9W pool 1: 758280-760583, 772104-774407 Soares NBHP pool 1: 304776-306311, 320136-322823, 326280-326663 Soares NBHOT pool 1: 723720-726407, 739080-740999 Subtraction by Bento Soares and M. Fatima Bonaldo."

BASE COUNT 97 a 142 c 146 g 128 t

ORIGIN

Query Match 20.8%; Score 513; DB 148; Length 513;
Best Local Similarity 100.0%; Pred. No. 2.5e-250;
Matches 513; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

97 atgacctccacccctccagcttccagtttccagtttgagagcattagatgagcccaagaa 156
DB 513 ATGACCTCACCCCTCCAGCTCTCCAGTTTCAGGTGAGAGCATTAGATGAGGCCAAGAA 454

157 gatgctctgagcgagacagaaagctgatttggagcgcgctccctccatgagag 216
DB 453 GATGGCTCTGAGCGGAGCAGAGAAAGCTGATTGGAGCGCGCTCCCTCCATGAGAG 394

217 tcacagttccagggcgagagacggaattccgcccctcagataagagtaaacctcaactac 276
DB 393 TCACAGTTCCAGGGCGAGACCGGAAATTCGCCCTCAGATAAGAGTCAACCTCAACTAC 334

277 cgaagaaggagacagtgctcagctcagcgatcccaaccgatttgaccgagatcggtcttc 336
DB 333 CGAAAGGAGACAGGTGCCAGCTGACCGGATCCAAACCGATTTCACCGAATCGGCTCTTC 274

337 aatcggtctcccgagggttcccccagagatctgctgagacttccagagtaacctgagcaag 396
DB 273 AATGCGGTCTCCCGGGGTGTCCCGAGATCTGGCTGAGACTTCCAGAGTAACCTGAGCAAG 214

397 accagcaagtacctcagcagactcggaaatacaagagggctccacaggttaagacgtgctg 456
DB 213 ACCAGCAAGTACTCTCACCACTCGGAATACACAGAGGCTCCACAGATGAAGAGTCCCTG 154

457 atgaagaagtgctcgtgaccttaagagcggagtaacgtcgtgatttctgcaactgtcgag 516
DB 153 ATGAAGAAGTGCTGTAACCTTAAGAGCGAGTCAATGCTGCTGCAATTCGTGCACGTGCGAG 94

517 atcgacaaggactctgagcaatccctcagcccctgtaaatgagccaggtgacagatgactat 576
DB 93 ATCGACAGGAGACTCTGGCAATCCTCAGCCCTGCTGTAAGAGCCCATGTGCACAGATGACTAT 34

577 taacgagggcacaagcgtctgacatcgccatt 609
DB 33 TACCGAGGCCACAGCGCTCTGCACATCGCCATT 1

RESULT 6
LOCUS A1126236 480 bp mRNA EST 27-OCT-1998
DEFINITION qc5a11.x1 Soares-placenta.8to9weeks.2NBHP8to9W Homo sapiens cDNA
clone IMAGE:1713500 3' similar to TR:035433 035433 VANILLOID
RECEPTOR SUBTYPE 1.; mRNA sequence.

ACCESSION A1126236
VERSION A1126236.1 GI:3594750
KEYWORDS EST;
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 480)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaps-remail.nih.gov
This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 1004 Std Error: 0.00
Seq primer: -40m13 fwd. ET from Amersham
High quality sequence stop: 450.
Location/Qualifiers
1. 480
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1713500"
/dev_stage="two placenta: one from 8 weeks and another from 9 weeks post conception"
/lab_host="DH10B (ampicillin resistant)"
/note="Organ: placenta; Vector: pRT3D (Pharmacia) with a modified polylinker; Site: 1: Not I; Site: 2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer (5' TGTACCAATCTGAAGTGGAGCGGCGCGGATTTTCTTTTCTTTT 3') double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pRT3 vector (Pharmacia). Library constructed by Bento Soares and M. Fatima Bonaldo."

BASE COUNT 90 a 139 c 133 g 118 t

ORIGIN

Query Match 19.4%; Score 480; DB 16; Length 480;
Best Local Similarity 100.0%; Pred. No. 1.7e-233;
Matches 480; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

182 agctgagatttggagcggtgctgctcccatgagtcacagttccagggcgagaccgga 241
DB 480 AGCTGAGATTTTGGAGCGGTGCTGCTCCCATGAGTCACAGTTCCAGGGCGAGACCGGA 421

242 aattcgccctcagataagagtaaacctcaactaccgaaaggagaggtgccaagtcagc 301
DB 420 AATTGCCCCCTCAGATTAAGTCAACCTCACTACCGAAAGGAGACAGTGCAGTCAAGC 361

302 cggatccaaacgatttgacagagatcggtcttcaatgcttcccggtgtgtccgcg 361
DB 360 CGGATCCAAACGATTGACCGAGATCGGCTCTTAATCGGCTCCCGGGGTGTCGCCG 301

363 aggatctgctgacttccagagtaacctcaggaagacgaagtaacctaccagctcg 421
DB 300 AGGATCTGGCTGACTTCCAGAGTACCTGAGCAAGCCAGCAATGACTCCAGCACTCGG 241

422 aatacagaagggtccacaggttaagagctgctgataagagctgtgcaaccttaag 481
DB 240 AATAACAGAGGCTCCACAGTAAAGACTGCTGATGAAGCTGTGTAACCTTAAGG 181

482 acgaggaatgctgcatcttgcacatgctgacagtcagacagaggaactgtgcaatctc 541
DB 180 ACGAGGTAATGCTGCAATTCGACACGCTCAGATGACAGAGGACTGTGCAATTCCTC 121

542 agcccttgtaattcccaatgacagatgactattaccagagccacagcgtctgcaca 601
DB 120 AGCCCTGTGTAATGCCAGTGCACAGATGACTATTACGAGGCGCACAGCGCTGTGCACA 61

Oy	602	tgcgcatctgaagaaggaaatcgtcaactgtgttaagtcctctgtgtgaagtggccaatg	661
Dd	60	tgcgcatctgaagaaggaaatcgtcaactgtgttaagtcctctgtgtgaagtggccaatg	1
RESULT	7		
AI801897/c			
LOCUS			
DEFINITION	AI801897	616 bp mRNA	EST 16-DEC-1999
		tx28ho2.x1 NCI-CGAP Lu24 Homo sapiens cDNA clone IMAGE:2270931 3'	
		similar to TR:O35433 O35433 VANILLOID RECEPTOR SUBTYPE 1 ;, mRNA	
sequence.			
ACCESSION	AI801897		
VERSION	AI801897.1	GI:5367369	
KEYWORDS	EST.		
SOURCE	human.		
ORGANISM	Homo sapiens		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.		
REFERENCE	1 (bases 1 to 616)		
AUTHORS	NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.		
JOURNAL	National Cancer Institute, Cancer Genome Anatomy Project (CGAP),		
TITLE	Tumor Gene Index		
COMMENT	Unpublished (1997)		
	Contact: Robert Strausberg, Ph.D.		
	Email: cgapbs-jemail.nih.gov		
	Tissue Procurement: Christopher Moskalko, M.D., Ph.D., Michael R.		
	Emmert-Buck, M.D., Ph.D.		
	cDNA Library Preparation: M. Bento Soares, Ph.D.		
	cDNA Library Arrayed by: Greg Lennon, Ph.D.		
	DNA sequencing by: Washington University Genome Sequencing Center		
	clone distribution: NCI-CGAP clone distribution information can be		
	found through the I.M.A.G.E. Consortium/LNLB at:		
	www.bio.lnlnl.gov/bhrp/image/image.html		
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	Seq primer: -400P from Glbco		
	High quality sequence stop: 456.		
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	/db_xref="taxon:9606"		
	/clone="IMAGE:2270931"		
	/clone_1id="NCI-CGAP_Lu24"		
	/tissue_type="carcinoid"		
	/lab_host="DH10B"		
	/note="Organ: lung; Vector: pT7D-Pac (Pharmacia) with a		
	modified polylinker. Plasmid DNA from the normalized		
	library NCI-CGAP_Lu5 was prepared, and ss circles were		
	made in vitro. Following HAP purification, this DNA was		
	used as tracer in a subtractive hybridization reaction.		
	The driver was PCR-amplified cDNAs from a pool of 5,000		
	clones made from the same library (clonoids		
	1414920-1417991 and 1520904-1522439). Subtraction by Bento		
	Soares and M. Fatima Bonaldo."		
BASE COUNT	129 a 189 c 169 g 128 t	1 others	
ORIGIN			
Query Match	19.4%; Score 479; DB 102; Length 616;		
Best Local Similarity	99.7% Pred. No. 5.6e-233;		
Matches 579; Conservative	0; Mismatches 2; Indels 0; Gaps 0;		
OY	1888	tttgagctcttcaattcacatcgcatgagcagctgagcttcacagagacagctgcac	1947
Dd	616	TTTGAGCTCTTCAATTCAATCACCATGGCATGGCCAGCTGCCTTCACAGACACTGCAC	557
OY	1948	tttcggcgagctgctgctgctgctgctgctggcctaagtgctgctcacctacatccctg	2007
Dd	556	TTTCGGCGAGCTGCTGCTGCTGCTGCTGCTGCCCTACGCTGNTGTACCTACATCTCTG	497
OY	2008	ctcaaacatgctcatcgcgccatcagagagacgctcaaacagtgctgcgaactgagacgtg	2067
Dd	496	CTCAACAATGCTCATCGCCCTCATGAGCGAAGCCGTCAAACAAGTGTGGCACACTGACAGCTGG	437

QY	2068	agacttggaaagcttgagaagaagcaccatctctgtcccttgagatgtgagaatggtctatgtgtg	2127
Db	436	AGCATGTGAAAGCTGCAGAAAGCCATCTGCTCTGTCTGAGATGAGAAATGGCTATTGTGTG	377
QY	2128	tgcagaagaagaagcagcagggcaggtgtgatgtctacccgtttgcacaaagcagatgtgcag	2187
Db	376	TGCAGAGAAAGACGACGGGGCAGGTGTGATGCTACCGTTTGCACTTAAGCCAGATGGCGCG	317
QY	2188	cggatgatcgcgtgtgtgtctcagggttgagagaggtgaacttggcttcattggagacagc	2247
Db	316	CCGGATGACGCGCTGCTGCTTCAAGAGGTGAGAGAGTGTAACATGGGCTTCATGTGGAGACG	257
QY	2248	ctggcctaacgctgtgtgagagaccgcgttaagggcagcaggtgtcccttgaactctgaaacct	2307
Db	256	CTGGCTACGCTGTGTGAGAACCCGCTGAGGGCGCGGTGCTCTCGAAGCTCTCGAAGACCC	197
QY	2308	gtccctgtctccctccctcccaaggagatgagatggtgtcctctgagaaaaactatgtggcc	2367
Db	196	GTCTGTGCTTCCCTCCCTCCCAAGAGATGAGATGTCCTCTGAGGAAAACTATTGTGGCC	137
QY	2368	gtccagctccctccagttccaatgatgtgtgcccagatgacagagagcagagacagagca	2427
Db	136	GTCCAGCTCCTCCAGTCCAACTGATGATGGCCCATGTCAGAGAGGCCAAGACAGACAGTA	77
QY	2428	gaggatcttcccaaccaatctgtgtgtcgtgtgggtccag	2468
Db	76	GAGGATCTTCCACACCACATCTGTGGCTGTGGGGTCCAG	36
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LOCUS	AA741232/c		
DEFINITION	AA741232.1	EST. 107-FEB-1998	
ACCESSION	AA741232.1	GI:2779824	
VERSION	1		
KEYWORDS	EST.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
TITLE	1 (bases 1 to 454)		
JOURNAL	NCI-CGAP htcp://www.ncbi.nlm.nih.gov/ncicgap.		
COMMENT	National Cancer Institute, Cancer Genome Anatomy Project (CGAP),		
	Unpublished (1997)		
	Contact: Robert Strausberg, Ph.D.		
	Email: cgaps-remail.nih.gov		
	Tissue Procurement: Louis M. Staudt, M.D., Ph.D., David Allman,		
	Ph.D., Gerald Marti, M.D.		
	CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima		
	Bonaldo, Ph.D.		
	CDNA Library Arrayed by: Greg Lennon, Ph.D.		
	DNA sequencing by: Washington University Genome Sequencing Center		
	Clone distribution: NCI-CGAP clone distribution information can be		
	found through the I.M.A.G.E. Consortium/ILNI at:		
	www.bio.lni.gov/bdrrp/image/image.html		
	Insert length: 692 Std Error: 0.00		
	Seq primer: -40ml3 fwd. ER from Amersham		
	High quality sequence stop: 424.		
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	/tissue_type="germinal center B cell"		
	/lab_host="DH10B"		
	/note="Vector: pT73D-Pac (Pharmacia) with a modified		
	polylinker. Site 1: Not I; Site 2: Eco RI; 1st strand cDNA		
	was prepared from human tonsillar cells enriched for		
	germinal center B cells by flow sorting (CD20+, IgD-),		
	provided by Dr. Louis M. Staudt (NCI), Dr. David Allman		

ORGANISM	Human sapiens
Euarchyonta: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
REFERENCE	1 (bases 1 to 481)
AUTHORS	NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap .
TITLE	National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL	Unpublished (1997)
COMMENT	Contact: Robert Strausberg, Ph.D. Email: cga@bbs-remail.nih.gov This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Insert Length: 818 Std Error: 0.00 Seq primer: -40m13 fwd. ET from Amersham High quality sequence stop: 159.
FEATURES	Location/Qualifiers 1..481 /organism="Homo sapiens" /db_xref="taxon:9606" /clone="IMAGE:1628595" /clone_lib="Soares_NRL_T_GBC_S1" /lab_host="DH10B" /note="Organ: pooled. Vector: pT73D-Pac (Pharmacia) with a modified polylinker. Site_1: Not I; Site_2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (fetal lung NBH119W, testis NHT, and B-cell NCI-GAP-GCBI) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 297480-302087, 682632-687239, 726408-728711, and 729096-731399. Subtraction by Bento Soares and M. Fatima Bonaldo."
BASE COUNT	96 a 152 c 119 g 114 t
ORIGIN	
Query Match	17.8%; Score 440; DB 14; Length 481;
Best Local Similarity	100.0%; Pred. No. 4.5e-213;
Matches 440; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
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DB 480	tgagggagaccgtcaacagctgtcgcactgacagctgtgaagcatctgtgaagctgcagaag 421
QY 2090	ccatctcgtctcctgagagtgaagaaagtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 2149
DB 420	ccatctcgtctcctgagagtgaagaaagtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 361
QY 2150	gtgtgatactgcagccgtgtgtgcaactaaagcagatgtgcagcccgatgtagctgtgtgttca 2209
DB 360	gtgtgatactgcagccgtgtgtgcaactaaagcagatgtgcagcccgatgtagctgtgtgttca 301
QY 2210	ggatggagagaggtgaactgtggcttcattgtggagagagagagctgctaagctgtgtgtgtgtgt 2269
DB 300	ggatggagagaggtgaactgtggcttcattgtggagagagagagctgctaagctgtgtgtgtgtgt 241
QY 2270	cgtcagggcagatgtccctcctcgaactctcgaagaccctgtctcctgtcctccctcccaagg 2329
DB 240	cgtcagggcagatgtccctcctcgaactctcgaagaccctgtctcctgtcctccctcccaagg 181
QY 2330	agagatggagatgtgtgtcctctgaggaataactgtgtcccgctccagctcctccagttcaact 2389
DB 180	agagatggagatgtgtgtcctctgaggaataactgtgtcccgctccagctcctccagttcaact 121
QY 2390	gatgtgccagatgtgacagagagccagagagagagagagatcttccaaaccacatct 2449
DB 120	gatgtgccagatgtgacagagagccagagagagagagagatcttccaaaccacatct 61
QY 2450	gctgtgctctgtgtgtgtcccaagt 2469
DB 60	gctgtgctctgtgtgtgtcccaagt 41

RESULT 11	BF594605	486 bp	mRNA	EST	12-DEC-2000
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ACCESSION	BF594605				
VERSION	BF594605				
KEYWORDS	EST.				
SOURCE	human.				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
TITLE	1 (bases 1 to 486)				
JOURNAL	NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap .				
COMMENT	National Cancer Institute, Cancer Genome Anatomy Project (CGAP),				
	Tumor Gene Index				
	Unpublished (1997)				
	Contact: Robert Strausberg, Ph.D.				
	Email: cgapbs-remail.nih.gov				
	Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.				
	Emmert-Buck, M.D., Ph.D.				
	CDNA Library Preparation: M. Bento Soares, Ph.D.				
	CDNA Library Arrayed by: Greg Lennon, Ph.D.				
	DNA Sequencing by: Washington University Genome Sequencing Center				
	Clone distribution: NCI-CGAP clone distribution information can be				
	found through the I.M.A.G.E. Consortium/LNLB, send email to:				
	lnl@image.lnl.gov				
	Seq primer: -400P from Glbco				
	High quality sequence stop: 410.				
FEATURES	Location/Qualifiers				
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	/lab_host="DH10B"				
	/note="Organ: Kidney; Vector: pT73D-Pac (Pharmacia) with				
	a modified polylinker; Site:1: Not I; Site:2: Eco RI;				
	Plasmid DNA from the normalized library NCI-CGAP_K1d3 was				
	prepared, and ss circles were made in vitro. Following RAP				
	hybridization, this DNA was used as tracer in a subtractive				
	hybridization reaction. The driver was PCR-amplified cDNAs				
	from a pool of 5,000 clones made from the same library				
	(cloneIDs 1322376-1323911, 1456007-1456775, and				
	1500552-1502855). Subtraction by Bento Soares and M.				
	Fatima Bonaldo."				
BASE COUNT	95 a 134 c 134 g 123 t				
ORIGIN					
Query Match	17.1%; Score 421; DB 151; Length 486;				
Best Local Similarity	100.0%; Freq. NO. 2.2e-203;				
Matches 421; Conservative	0; Mismatches 0; Indels 0; Gaps 0;				
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Db 421	CGCCCTCAGATTAAGAGTCAACCTCAACTACCGAAGGAAGCAAGTCCAGTCAGCCGGA 362				
Y 306	tccaacccgatttgcagcagagatcggtcttcaatgacggtcccgagggtgtccccagga 365				
Db 361	TCCAAACCGATTTCACCGAGATCGGCTTTTAAAGCGGCTCCCGGGGTGTGCCCGAGGA 302				
Y 366	tctgctgacttcagagtgatcctcgagcaagaacagcaagtaactcaaccgactcgagata 425				
Db 301	TCTGCTGGAATTCACAGATACCTGAGCAAGACCAAGCAAGTACTCACCGACTCGGATA 242				
Y 426	cacagagggctccacaggtaaagacgtgcctgatagaagctgtgtcgaaccttaagagcgg 485				
Db 241	CACGAGGGCTCCACAGGTAAAGACGTGCTGATGAAGGCTGTGCTGAACCTTAAGGACGG 182				

TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
JOURNAL Tumor Gene Index
COMMENT Unpublished (1997)
 Contact: Robert Strausberg, Ph.D.
 Email: cgaps-rt@mail.nih.gov
 Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.
 CDNA Library Preparation: M. Bento Soares, Ph.D.
 DNA Library Arrayed by: Greg Lennon, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www.bio.llnl.gov/bdrrp/image/image.html
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 High quality sequence stop: 426.
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 /lab_host="DH10B"
 /note="Organ: kidney; Vector: p7T73D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Plasmid DNA from the normalized library NCI-CGAP_Kid3 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneids 1322376-1323911, 1436007-1456775, and 1500352-1502855). Subtraction by Bento Soares and M. Fatima Bonaldo."

BASE COUNT 80 a 116 c 126 g 106 t
ORIGIN

Query Match 16.6%; Score 410; DB 24; Length 428;
 Best Local Similarity 100.0%; Pred. No. 9.2e-198;
 Matches 410; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 200 ggctgcctccatgagtcacgttcagggcgagggcgaaattcgccctcagataa 259
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 DB 410 ggctgcctccatgagtcacgttcagggcgagggcgaaattcgccctcagataa 351
 |||
 QY 260 gaatcaacctcaactccgaaggaaggaagtgccagtcagccgacccaacgattg 319
 |||
 DB 350 gactcaacctcaactccgaaggaaggaagtgccagtcagccgacccaacgattg 291
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 QY 320 accgagatcggtctcctcaatgctcccgagggtgtcccgagagatctgctgactc 379
 |||
 DB 290 accgagatcggtctcctcaatgctcccgagggtgtcccgagagatctgctgactc 231
 |||
 QY 380 caaagtaacctggaacgaagacgaagtaactcaccgagctcggaatacagaagggctca 439
 |||
 DB 230 caaagtaacctggaacgaagacgaagtaactcaccgagctcggaatacagaagggctca 171
 |||
 QY 440 caagtaagacgttcctgataaagctgtgtgtaaccttaaggaacggagtgtaagccctgca 499
 |||
 DB 170 caagtaagacgttcctgataaagctgtgtgtaaccttaaggaacggagtgtaagccctgca 111
 |||
 QY 500 ttctgcacatctgtcagatcgacagaggaactctgcaatcctcagccctgttaatgcc 559
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 DB 110 ttctgcacatctgtcagatcgacagaggaactctgcaatcctcagccctgttaatgcc 51
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 QY 560 atgtccacatgtactattaccgaagcccaagcgctctgcaatcgccatt 609
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 DB 50 atgtccacatgtactattaccgaagcccaagcgctctgcaatcgccatt 1
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RESULT 14
 AM467012/c
 LOCUS AM467012 512 bp mRNA EST 24-FEB-2000

DEFINITION ha07e10.x1 NCI-CGAP_Kid12 Homo sapiens CDNA clone IMAGE:2873034 3' similar to TR:035433 035433 VANILLOID RECEPTOR SUBTYPE 1. ; mRNA sequence.
ACCESSION AM467012
VERSION AM467012.1 GI:7037118
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 512)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgaps-rt@mail.nih.gov
 Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.
 CDNA Library Preparation: M. Bento Soares, Ph.D.
 DNA Library Arrayed by: Greg Lennon, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www.bio.llnl.gov/bdrrp/image/image.html
 Seq primer: -400P from Glibco
 High quality sequence stop: 441.
FEATURES
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 /tissue_type="2-pooled tumors (clear cell type)"
 /lab_host="DH10B"
 /note="Organ: kidney; Vector: p7T73D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Plasmid DNA from the normalized library NCI-CGAP_Kid3 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneids 1492104-1493255). Subtraction by Bento Soares and M. Fatima Bonaldo."

BASE COUNT 94 a 151 c 139 g 128 t
ORIGIN

Query Match 16.6%; Score 410; DB 116; Length 512;
 Best Local Similarity 99.6%; Pred. No. 9.2e-198;
 Matches 510; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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 DB 512 agacattagatggaggcgaagatgctctgagcgagcagaagaaactgtgatttg 453
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 QY 194 gtagcgagctgcgtctccatgagatcaggttcagagtcagcgagatcccaacc 253
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 DB 452 gtagcgagctgcgtctccatgagatcaggttcagagtcagcgagatcccaacc 193
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 QY 254 agataagatcaacctcaactaccgaaggaaggaagtgccagtcagcgagatcccaacc 313
 |||
 DB 392 agataagatcaacctcaactaccgaaggaaggaagtgccagtcagcgagatcccaacc 333
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 QY 314 gatttcacagatcggtctcctcaatgagtcctccggagggtgtcccgagagatcgctg 373
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 DB 332 gatttcacagatcggtctcctcaatgagtcctccggagggtgtcccgagagatcgctg 273
 |||
 QY 374 gacttcacagatcctgtgagcaagacgaagtaactcaccgagctcggaatacagaag 433
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 DB 272 gacttcacagatcctgtgagcaagacgaagtaactcaccgagctcggaatacagaag 213
 |||

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: October 4, 2001, 09:08:15 ; Search time 80.95 Seconds
(without alignments)
5774.048 Million cell updates/sec

Title: US-09-445-614-1

Perfect score: 2469
Sequence: 1 caccagagcgacgcgcagct.....gctgctctgggtccagcagt 2469

Scoring table: OLIGO-MNC
Gapop 60.0 , Gapext 60.0

Searched: 324599 seqs, 9465562 residues

Word size : 0

Total number of hits satisfying chosen parameters: 649198

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

Issued Patents, NA: *
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2: /cgn2.6/ptodata/1/lna/5B.COMB.seq:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	27	1.1	3500	4	US-09-197-636-7
2	27	1.1	4803	4	US-09-197-636-1
3	27	1.1	4803	4	US-09-197-636-3
4	20	0.8	506	1	US-08-469-802B-7
5	20	0.8	506	2	US-08-469-802B-7
6	20	0.8	1173	2	US-08-468-819-88
7	20	0.8	2201	3	US-09-330-970-2
8	20	0.8	2461	1	US-08-282-141-1
9	20	0.8	3336	3	US-09-330-970-4
10	19	0.8	43	2	US-08-531-927B-17
11	19	0.8	168	1	US-08-469-802B-4
12	19	0.8	168	2	US-08-267-803B-4
13	19	0.8	168	2	US-08-569-147-90
14	19	0.8	171	1	US-08-469-802B-5
15	19	0.8	171	2	US-08-267-803B-5
16	19	0.8	195	1	US-08-469-802B-2
17	19	0.8	234	1	US-08-267-802B-3
18	19	0.8	234	2	US-08-469-802B-3
19	19	0.8	510	2	US-08-267-803B-3
20	19	0.8	510	2	US-08-184-009-150
21	19	0.8	510	2	US-08-458-356-150
22	19	0.8	619	6	5273901-4
23	19	0.8	619	6	5482709-3
24	19	0.8	2036	3	US-08-923-454A-17
25	19	0.8	2065	3	US-08-335-865J-8
26	19	0.8	2205	3	US-08-888-077A-41
27	19	0.8	2214	3	US-08-864-038A-1

C 28	19	0.8	2584	3	US-08-758-662-8	Sequence 8, Appl
C 29	19	0.8	3132	2	US-08-224-482-3	Sequence 3, Appl
C 30	19	0.8	3132	3	US-09-205-921-1	Sequence 1, Appl
C 31	19	0.8	3331	3	US-08-864-038A-2	Sequence 2, Appl
C 32	19	0.8	3331	3	US-08-864-038A-4	Sequence 4, Appl
C 33	19	0.8	3366	1	US-08-469-802B-1	Sequence 1, Appl
C 34	19	0.8	3366	2	US-08-267-803B-1	Sequence 1, Appl
C 35	19	0.8	10660	4	US-08-467-803B-8	Sequence 8, Appl
C 36	19	0.8	10660	4	US-09-041-886-16	Sequence 16, Appl
C 37	19	0.8	50937	4	US-09-428-517-1	Sequence 1, Appl
C 38	18	0.7	52	4	US-09-332-769-3	Sequence 3, Appl
C 39	18	0.7	72	1	US-08-446-102-3	Sequence 3, Appl
C 40	18	0.7	78	1	US-08-446-102-1	Sequence 1, Appl
C 41	18	0.7	78	1	US-08-446-102-2	Sequence 2, Appl
C 42	18	0.7	78	4	US-08-617-010C-15	Sequence 15, Appl
C 43	18	0.7	78	4	US-09-566-591-15	Sequence 15, Appl
C 44	18	0.7	106	2	US-08-613-233-15	Sequence 15, Appl
C 45	18	0.7	117	6	5273901-8	Patent No. 5273901

ALIGNMENTS

RESULT 1
US-09-197-636-7
; Sequence 7, Application US/09197636
; Patent No. 6239267
GENERAL INFORMATION:
APPLICANT: DUCKWORTH, DAVID
APPLICANT: HAYES, PHILIP
APPLICANT: MEADOWS, HELEN
APPLICANT: DAVIS, JOHN
TITLE OF INVENTION: NOVEL COMPOUNDS
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ratner & Prestia
STREET: P.O. Box 980
CITY: Valley Forge
STATE: PA
COUNTRY: US
ZIP: 19482-0980
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/197,636
FILING DATE: 23-NOV-1998
CLASSIFICATION:
Prior Application DATA:
APPLICATION NUMBER: UK 9805137.8
FILING DATE: 12-MAR-1998
APPLICATION NUMBER: UK 9815791.0
FILING DATE: 21-JUL-1998
APPLICATION NUMBER: UK 9819278.4
FILING DATE: 03-SEP-1998
ATTORNEY/AGENT INFORMATION:
NAME: Prestia, Paul F
REGISTRATION NUMBER: 23,031
REFERENCE/DOCKET NUMBER: GP-30075
TELECOMMUNICATION INFORMATION:
TELEPHONE: 601-407-0700
TELEFAX: 610-407-0701
TELEX: 846169
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 3500 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-09-197-636-7

Query Match 1.1%; Score 27; DB 4; Length 3500;
Best Local Similarity 100.0%; Pred. No. 0.0029;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2005 ctgctcaacatgctcctcctcatg 2031
|||||
DB 2886 ctgctcaacatgctcctcctcatg 2912

RESULT 2

US-09-197-636-1

; Sequence 1, Application US/09197636
; Patent No. 6239267
; GENERAL INFORMATION:

APPLICANT: DUCKWORTH, DAVID

APPLICANT: HAYES, PHILIP

APPLICANT: MEADOWS, HELEN

APPLICANT: DAVIS, JOHN

TITLE OF INVENTION: NOVEL COMPOUNDS

NUMBER OF SEQUENCES: 8

CORRESPONDENCE ADDRESS:

ADDRESSEE: Ratner & Prestia

STREET: P.O. Box 980

CITY: Valley Forge

STATE: PA

COUNTRY: US

ZIP: 19482-0980

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FASTSEQ for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/197,636

FILING DATE: 23-NOV-1998

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: UK 9805137.8

FILING DATE: 12-MAR-1998

APPLICATION NUMBER: UK 9815791.0

FILING DATE: 21-JUL-1998

APPLICATION NUMBER: UK 9819278.4

FILING DATE: 03-SEP-1998

ATTORNEY/AGENT INFORMATION:

NAME: Prestia, Paul F

REGISTRATION NUMBER: 23,031

REFERENCE/DOCKET NUMBER: GP-30075

TELECOMMUNICATION INFORMATION:

TELEPHONE: 601-407-0700

TELEFAX: 610-407-0701

TELEX: 846169

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 4803 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: CDNA

US-09-197-636-1

Query Match 1.1%; Score 27; DB 4; Length 4803;
Best Local Similarity 100.0%; Pred. No. 0.0029;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2005 ctgctcaacatgctcctcctcatg 2031
|||||
DB 2886 ctgctcaacatgctcctcctcatg 2912

RESULT 3

US-09-197-636-3
; Sequence 3, Application US/09197636
; Patent No. 6239267
; GENERAL INFORMATION:

APPLICANT: DUCKWORTH, DAVID

APPLICANT: HAYES, PHILIP

APPLICANT: MEADOWS, HELEN

APPLICANT: DAVIS, JOHN

TITLE OF INVENTION: NOVEL COMPOUNDS

NUMBER OF SEQUENCES: 8

CORRESPONDENCE ADDRESS:

ADDRESSEE: Ratner & Prestia

STREET: P.O. Box 980

CITY: Valley Forge

STATE: PA

COUNTRY: US

ZIP: 19482-0980

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FASTSEQ for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/197,636

FILING DATE: 23-NOV-1998

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: UK 9805137.8

FILING DATE: 12-MAR-1998

APPLICATION NUMBER: UK 9815791.0

FILING DATE: 21-JUL-1998

APPLICATION NUMBER: UK 9819278.4

FILING DATE: 03-SEP-1998

ATTORNEY/AGENT INFORMATION:

NAME: Prestia, Paul F

REGISTRATION NUMBER: 23,031

REFERENCE/DOCKET NUMBER: GP-30075

TELECOMMUNICATION INFORMATION:

TELEPHONE: 601-407-0700

TELEFAX: 610-407-0701

TELEX: 846169

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 4803 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: CDNA

US-09-197-636-3

Query Match 1.1%; Score 27; DB 4; Length 4803;
Best Local Similarity 100.0%; Pred. No. 0.0029;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2005 ctgctcaacatgctcctcctcatg 2031
|||||
DB 2886 ctgctcaacatgctcctcctcatg 2912

RESULT 4

US-08-469-802B-7/C

; Sequence 7, Application US/08469802B
; Patent No. 5741645
; GENERAL INFORMATION:

APPLICANT: Orr, Harry T.

APPLICANT: Rannum, Laura P.W.

APPLICANT: Chung, Ming-Yi

APPLICANT: Zoghbi, Huda Y.

TITLE OF INVENTION: Gene Sequence for Spinocerebellar Ataxia

Patent No. 5741645

TITLE OF INVENTION: Type 1 and Method for Diagnosis

NUMBER OF SEQUENCES: 47

CORRESPONDENCE ADDRESS:
ADDRESSEE: Muehling, Raasch, Gebhardt & Schwappach, P.A.
STREET: 119 No. 5741645th Fourth Street, Suite 203
CITY: Minneapolis
STATE: MN
COUNTRY: USA
ZIP: 55401
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/469,802B
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Muehling, Ann M. 33,977
REGISTRATION NUMBER: 33,977
REFERENCE/DOCKET NUMBER: 110,00030101
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-305-1217
TELEFAX: 612-305-1225
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 506 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-469-802B-7

Query Match
Best Local Similarity 100.0%; Pred. No. 5.3;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1958 tggctgctgctgctgctg 1977
|||||
Db 233 TGGTGGCTGCTGCTGCTG 214

RESULT 5
US-08-267-803B-7/c
Sequence 7 Application US/08267803B
Patent No. 5834183
GENERAL INFORMATION:
APPLICANT: Ott, Harry T.
APPLICANT: Ranum, Laura P.W.
APPLICANT: Chung, Ming-Yi
APPLICANT: Zoghbi, Huda Y.
TITLE OF INVENTION: Gene Sequence for Spino cerebellar Ataxia
Patent No. 5834183
TITLE OF INVENTION: Type 1 and Method for Diagnosis
NUMBER OF SEQUENCES: 85
CORRESPONDENCE ADDRESS:
ADDRESSEE: Muehling, Raasch, Gebhardt & Schwappach, P.A.
STREET: P.O. Box 581415
CITY: Minneapolis
STATE: MN
COUNTRY: USA
ZIP: 55458-1415
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/267,803B
FILING DATE: 28-JUN-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: McCormack, Myra H.

REGISTRATION NUMBER: 36,602
REFERENCE/DOCKET NUMBER: 110,00030120
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-305-1217
TELEFAX: 612-305-1228
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 506 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-267-803B-7

Query Match
Best Local Similarity 100.0%; Pred. No. 5.3;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1958 tggctgctgctgctgctg 1977
|||||
Db 233 TGGTGGCTGCTGCTGCTG 214

RESULT 6
US-08-468-819-88
Sequence 88 Application US/08468819
Patent No. 5871723
GENERAL INFORMATION:
APPLICANT: Strieter, Robert M.
APPLICANT: Polverini, Peter J.
APPLICANT: Kunkel, Steven L.
TITLE OF INVENTION: CXG Chemokines as Regulators of
TITLE OF INVENTION: CXG Chemokines as Regulators of
NUMBER OF SEQUENCES: 93
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: US
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/468,819
FILING DATE: Concurrently herewith
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Highlander, Steven L.
REGISTRATION NUMBER: 37,642
REFERENCE/DOCKET NUMBER: UMIC:003/HYL
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512/418-3000
TELEFAX: 512/474-7477
TELEX: N/A
INFORMATION FOR SEQ ID NO: 88:
SEQUENCE CHARACTERISTICS:
LENGTH: 1173 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "DNA"
US-08-468-819-88

Query Match
Best Local Similarity 100.0%; Pred. No. 5.1;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;


```
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/531,927B
FILING DATE: 21-SEP-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP H6-251600
FILING DATE: 21-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: ATH95-01A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-861-6240
TELEFAX: 617-861-9540
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 43 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-531-927B-17

Query Match
Best Local Similarity 100.0%; Pred. No. 17;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1961 tctgtctgtctgtctgtcgc 1979
|||||
Db 10 TGCTGCTGCTGCTGCTGCTGC 28

RESULT 11
US-08-469-802B-4/C
Sequence 4, Application US/08469802B
Patent No. 5741645
GENERAL INFORMATION:
APPLICANT: Orr, Harry T.
APPLICANT: Rannum, Laura P.W.
APPLICANT: Chung, Ming-Yi
APPLICANT: Zoghbi, Huda Y.
TITLE OF INVENTION: Gene Sequence for Spinocerebellar Ataxia
Patent No. 5741645
TITLE OF INVENTION: Type 1 and Method for Diagnosis
NUMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESS:
ADDRESSEE: Muelling, Raasch, Gebhardt & Schwappach, P.A.
STREET: 119 No. 5741645th Fourth Street, Suite 203
CITY: Minneapolis
STATE: MN
COUNTRY: USA
ZIP: 55401
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/469,802B
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Muelling, Ann M.
REGISTRATION NUMBER: 33,977
REFERENCE/DOCKET NUMBER: 110.00030101
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-305-1217
TELEFAX: 612-305-1225
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
```

```
LENGTH: 168 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-469-802B-4
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```
Query Match
Best Local Similarity 100.0%; Pred. No. 16;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1959 ggtcgtcgtcgtcgtcgtc 1977
|||||
Db 145 GGTGCTGCTGCTGCTGCTG 127
```

```
RESULT 12
US-08-267-803B-4/C
Sequence 4, Application US/08267803B
Patent No. 5834183
GENERAL INFORMATION:
APPLICANT: Orr, Harry T.
APPLICANT: Rannum, Laura P.W.
APPLICANT: Chung, Ming-Yi
APPLICANT: Zoghbi, Huda Y.
TITLE OF INVENTION: Gene Sequence for Spinocerebellar Ataxia
Patent No. 5834183
TITLE OF INVENTION: Type 1 and Method for Diagnosis
NUMBER OF SEQUENCES: 85
CORRESPONDENCE ADDRESS:
ADDRESSEE: Muelling, Raasch, Gebhardt & Schwappach, P.A.
STREET: P.O. Box 581415
CITY: Minneapolis
STATE: MN
COUNTRY: USA
ZIP: 55458-1415
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/267,803B
FILING DATE: 28-JUN-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: McCormack, Myra H.
REGISTRATION NUMBER: 36,602
REFERENCE/DOCKET NUMBER: 110.00030120
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-305-1217
TELEFAX: 612-305-1228
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 168 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-267-803B-4
```

```
Query Match
Best Local Similarity 100.0%; Pred. No. 16;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1959 ggtcgtcgtcgtcgtcgtc 1977
|||||
Db 145 GGTGCTGCTGCTGCTGCTG 127
```

RESULT 13

US-08-569-147-90
; Sequence 90, Application US/08569147
; Patent No. 6180377
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: HUMANISED ANTIBODIES
; NUMBER OF SEQUENCES: 95
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/569,147
; FILING DATE: 25-March-1996
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Trujillo, Doreen Yatho
; REGISTRATION NUMBER: 35,719
; REFERENCE/DOCKET NUMBER: CARP-0047
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 90:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 168 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 16..168
; US-08-569-147-90

Query Match 0.8%; Score 19; DB 4; Length 168;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 211 atggagtcacgtccagg 229
|||||
Db 28 atggagtcacgtccagg 46

RESULT 14
US-08-469-802B-5/C
; Sequence 5, Application US/08469802B
; Patent No. 5741645
; GENERAL INFORMATION:
; APPLICANT: Ott, Harry T.
; APPLICANT: Rannum, Laura P.W.
; APPLICANT: Chung, Ming-Yi
; APPLICANT: Zoghbi, Huda Y.
; TITLE OF INVENTION: Gene Sequence for Spinocerebellar Ataxia
; Patent No. 5741645
; TITLE OF INVENTION: Type 1 and Method for Diagnosis
; NUMBER OF SEQUENCES: 47
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Muelting, Raasch, Gebhardt & Schwappach, P.A.
; STREET: 119 No. 5741645th Fourth Street, Suite 203
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55401

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/469,802B
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Muelting, Ann M.
; REGISTRATION NUMBER: 33,977
; REFERENCE/DOCKET NUMBER: 110.00030101
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612-305-1217
; TELEFAX: 612-305-1225
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 171 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; US-08-469-802B-5

Query Match 0.8%; Score 19; DB 1; Length 171;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1959 ggtgctgctgctgctgctg 1977
|||||
Db 148 ggtgctgctgctgctgctg 130

RESULT 15
US-08-267-803B-5/C
; Sequence 5, Application US/08267803B
; Patent No. 5834183
; GENERAL INFORMATION:
; APPLICANT: Ott, Harry T.
; APPLICANT: Rannum, Laura P.W.
; APPLICANT: Chung, Ming-Yi
; APPLICANT: Zoghbi, Huda Y.
; TITLE OF INVENTION: Gene Sequence for Spinocerebellar Ataxia
; Patent No. 5834183
; TITLE OF INVENTION: Type 1 and Method for Diagnosis
; NUMBER OF SEQUENCES: 85
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Muelting, Raasch, Gebhardt & Schwappach, P.A.
; STREET: P.O. Box 581415
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55458-1415
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/267,803B
; FILING DATE: 28-JUN-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: McCormack, Myra H.
; REGISTRATION NUMBER: 36,602
; REFERENCE/DOCKET NUMBER: 110.00030120
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612-305-1217
; TELEFAX: 612-305-1228
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:

LENGTH: 171 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-267-803B-5

Query Match 0.8%; Score 19; DB 2; Length 171;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1959 ggtgctgctgctgctgctg 1977
|||||
Db 148 GGTGCTGCTGCTGCTGCTG 130

Search completed: October 4, 2001, 11:13:47
Job time: 7532 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 4, 2001, 08:21:05 ; Search time 3271.04 Seconds
(without alignments)
11675.147 Million cell updates/sec

Title: US-09-445-614-1

Perfect score: 2469
Sequence: 1 caccagagccgacgcgcagct.....gctgctctggggtcccaagt 2469

Scoring table: OLIGO NUC
Gapop 60.0 , Gapext 60.0

Searched: 1344157 seqs, 7733874588 residues

Word size : 0

Total number of hits satisfying chosen parameters: 2688314

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

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9: gb_pat1:*
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11: gb_ph:*
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18: em_fun:*
19: em_hcgo_hum:*
20: em_hcgo_inv:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	2249	91.1	2351	9	AX019706 Sequence 1
3	2168	87.8	2783	9	AX017826 Sequence 1
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5	2057	83.3	2348	9	AX019710 Sequence 1
6	1340	54.3	2765	91	AX023769 Sequence 1
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VERSION AX019706.1 GI:10043549
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Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
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1 (bases 1 to 2351)
AUTHORS Duckworth,D.M., Davis,J.B. and Hayes,P.D.
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JOURNAL Patent: WO 937765-A 1 29-JUL-1999;
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 ACCESSION AX023795
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 KEYWORDS
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 REFERENCE 1 (bases 1 to 2765)
 AUTHORS England, S., Wood, J.N. and Garcia, R.
 TITLE Ion channels, in particular vanilloid receptor - like (vr-1)
 JOURNAL Patent: WO 0022121-A 20-APR-2000;
 UNIV LONDON (GB) ; ENGLAND STEVEN (GB) ; WOOD JOHN NICHOLAS (GB) ;
 GARCIA REYNALDO (PH)
 FEATURES
 source 1..2765
 Location/Qualifiers
 BASE COUNT 560 a 821 c 792 g 589 t 3 others
 ORIGIN
 Query Match 54.3%; Score 1340; DB 91; Length 2765;
 Best Local Similarity 99.1%; Pred. No. 0;
 Matches 2440; Conservative 0; Mismatches 22; Indels 0; Gaps 0;
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RESULT 8
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DEFINITION Homo sapiens vanilloid receptor-like protein (VRL) mRNA, complete cds.
ACCESSION AF103906
VERSION AF103906.1 GI:5305597
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
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AUTHORS 1 (bases 1 to 2507)
 Garcia, R.L., Delmas, P., Cesare, P., England, S., Lepil, A. and Wood, J.N.
TITLE Cloning and functional expression of VRL, a vanilloid receptor-like gene
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 2507)
AUTHORS Garcia, R.L. and Wood, J.N.
TITLE Direct Submission
JOURNAL Submitted (02-NOV-1998) Department of Biology, University College London, Gower St., London WC1E 6BT, United Kingdom
FEATURES Location/Qualifiers
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ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE 1 (bases 1 to 2713)
AUTHORS Ishibashi, K.
TITLE Molecular cloning of a stretch activated channel from rat kidney
JOURNAL Published Only in Database (1999) in press
REFERENCE 2 (bases 1 to 2713)
AUTHORS Ishibashi, K.
TITLE Direct Submission
JOURNAL Submitted (24-JUN-1999) to the DDBJ/EMBL/GenBank databases. Kenichi
Ishibashi, Jichi Medical School, Pharmacology; Minami-Kawachi,
Kawachi, Tochigi 329-0498, Japan (E-mail: kishibae@jichi.ac.jp,
Tel:81-285-58-7326, Fax:81-285-44-5541)
FEATURES
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OY 1648 cagcacacagcgtctacagtgcatgcatccagaagtcctc 1691
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LOCUS Rattus norvegicus vanilloid receptor-like protein 1 (VRL-1) mRNA,
DEFINITION complete cds.
ACCESSION AF129113
VERSION AF129113.1 GI:4589142
KEYWORDS
SOURCE Norway rat.
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE 1 (bases 1 to 2718)
AUTHORS Caterina, M.J., Rosen, T.A., Tomlinaga, M., Brake, A.J. and Julius, D.
TITLE A capsaicin-receptor homologue with a high threshold for noxious

JOURNAL Nature 398 (6726), 436-441 (1999)
MEDLINE 9921558
REFERENCE 2 (bases 1 to 2718)
AUTHORS Caterina, M.J., Rosen, T.A., Tomlinaga, M., Brake, A.J. and Julius, D.
TITLE Direct Submission
JOURNAL Submitted (17-FEB-1999) Cellular and Molecular Pharmacology,
University of California, 513 Parnassus, San Francisco, CA 94143,
USA
FEATURES
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BASE COUNT 597 a 780 c 728 g 613 t
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Query Match 1.8%; Score 44; DB 94; Length 2718;
Best Local Similarity 100.0%; Pred. No. 1.5e-12;
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1648 cagcacacagcgtctacagtgcatgcatccagaagtcctc 1691
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Db 1867 CAGCACACAGGATCTACAGTGTCATGATCAGAGGATCATCT 1930

RESULT 13
AB022332 2890 bp mRNA ROD 04-APR-2000
LOCUS Rattus norvegicus mRNA for ion channel from kidney, complete cds.
DEFINITION AB022332
ACCESSION AB022332.1 GI:7415516
VERSION AB022332.1 GI:7415516
KEYWORDS
SOURCE Rattus norvegicus male kidney cDNA to mRNA.
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE 1 (sites)
AUTHORS Suzuki, M.
TITLE Ion channel
JOURNAL Unpublished (1999)
REFERENCE 2 (bases 1 to 2890)
AUTHORS Suzuki, M.
TITLE Direct Submission
JOURNAL Submitted (12-JAN-1999) to the DDBJ/EMBL/GenBank databases. Makoto
Suzuki, Jichi Medical School, Pharmacology; 3311-1, Yakushiji,
Minamikawachi, Tochigi 329-0498, Japan (E-mail: mcsuz@jichi.ac.jp,
Tel:81-28-558-7336, Fax:81-28-544-5541)
Sequence updated (27-Apr-1999).


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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: October 3, 2001, 17:31:07 ; Search time 24.2 Seconds
(without alignments)
2064.222 Million cell updates/sec

Title: US-09-445-614-2

Sequence: 1 MTPSSSSVFRLRLTDGQOE.....EDEDGASEBNVYPVQLQSN 824

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 412676 seqs, 60623988 residues

Total number of hits satisfying chosen parameters: 412676

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

A-Geneseq 0601:*

1:	/SID88/gcgdata/geneseq/AA1980.DAT:*
2:	/SID88/gcgdata/geneseq/AA1981.DAT:*
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22:	/SID88/gcgdata/geneseq/AA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3964	90.6	764	20	AAV29469 Human vanilloid re
2	3964	90.6	764	20	AAV06559 Human vanilloid re
3	3964	90.6	764	21	AAV97358 Human VR-2 protein
4	3964	90.6	764	22	AAV35622 Human vanilloid re
5	3948.5	90.2	763	20	AAV42308 Human vanilloid re
6	3948.5	90.2	763	20	AAV29471 Human vanilloid re
7	3899	89.1	764	21	AAV84834 Human acid sequenc
8	3011.5	73.5	630	21	AAV97364 Human VR-2 (altern
9	3011.5	68.8	761	20	AAV06556 Rat vanilloid rece
10	2996.5	68.8	761	20	AAV99790 Rat VRRP-1 (VR2) c
11	2996.5	68.5	727	20	AAV06560 Human vanilloid re

12	2996.5	68.5	727	20	AAV99798
13	2240	51.2	436	21	AAV97359
14	2230	51.0	554	21	AAV97360
15	1649	37.7	843	20	AAV06561
16	1649	37.7	843	20	AAV97357
17	1628.5	37.2	839	21	AAV97357
18	1625.5	37.1	839	21	AAV96478
19	1621.5	37.1	839	20	AAV30155
20	1621.5	37.1	839	20	AAV06558
21	1621.5	37.1	839	21	AAV32127
22	1618	37.0	838	20	AAV06555
23	1618	37.0	838	20	AAV9789
24	1617.5	37.0	839	20	AAV30152
25	1615.5	36.9	839	-20	AAV30153
26	1440	32.9	279	19	AAV74908
27	1418	32.4	963	21	AAV96479
28	956.5	21.9	217	20	AAV29470
29	635	14.5	725	22	AAV00412
30	635	14.5	725	22	AAV00413
31	634	14.5	725	22	AAV31595
32	605.5	13.8	727	22	AAV31596
33	482.5	11.0	451	22	AAV00414
34	274	6.3	57	20	AAV99793
35	272	6.2	232	19	AAV75021
36	247	5.6	71	20	AAV99792
37	220.5	5.0	974	19	AAV55960
38	193	4.4	233	21	AAV74791
39	171.5	3.9	225	21	AAV36084
40	160	3.7	1700	21	AAV18144
41	155	3.5	1081	20	AAV24319
42	145.5	3.3	1095	20	AAV00931
43	144.5	3.3	1104	20	AAV95437
44	143	3.3	60	17	AAV98207
45	142.5	3.3	44	17	AAV98208

ALIGNMENTS

RESULT 1

ID AAV29469 standard; Protein; 764 AA.

AC AAV29469;

DT 08-OCT-1999 (first entry)

DE Human vanilloid receptor homologue VANILREP2.

KW Human; vanilloid receptor homologue; VANILREP2; polymorphic variant;

KW PVP-1; therapy; diagnosis; chronic pain; neuropathic; postoperative;

KW rheumatoid arthritis; neuralgia; algesia; nerve injury; ischemia;

KW neurodegeneration; stroke; incontinence; inflammatory disorder.

OS Homo sapiens.

PN MO9937765-A1.

PD 29-JUL-1999.

PF 25-JAN-1999; 99MO-EP00420.

PR 20-JAN-1999; 99GB-0001209.

PR 27-JAN-1998; 98BP-0300549.

PR 26-OCT-1998; 98GB-0023421.

PA (SMRK) SMITHKLINE BEECHAM PLC.

PI Davis JB, Duckworth DM, Hayes PD.

XX WPI: 1999-479049/40.

XX N-PSDB; AA207114.

XX DR

XX

PT New human vanilloid receptor homologues (VANILREP2)
 XX
 PS Claim 4; Page 30-32; 47pp; English.
 CC The present sequence represents a human vanilloid receptor homologue,
 CC designated VANILREP2. VANILREP2 can be used to diagnose disease or
 CC susceptibility to disease related to expression or activity of
 CC VANILREP2 polypeptides. VANILREP2 may be used to treat diseases
 CC including pain, (for example chronic, neuropathic, postoperative,
 CC rheumatoid arthritis), neuralgia, algisia, nerve injury, ischemia,
 CC neurodegeneration, stroke, incontinence, and inflammatory disorders.
 XX
 XX Sequence 764 AA:
 SO
 Query Match 90.6%; Score 3964; DB 20; Length 764;
 Best Local Similarity 92.7%; Pred. No. 0;
 Matches 764; Conservative 0; Mismatches 0; Indels 60; Gaps 1;
 QY 1 MTSFSSSPVRLERLDDGGEDSGADRGKIDFGSGLPMSQOGEDEKRAPIRVNLNY 60
 DB 1 mtspspsvrlrletldgggedsgadrgkldfgsglpmsqfgedrktapqrlrvnlly 60
 QY 61 RKGTGASQDPNFRDRLFNAYSRGVPGAGATCTGGCTGCACTCCAGATCACTGAG 120
 DB 61 rkgtgasqdpnfrdrlfnaysrgvpgagatctggctgcactccagatcactgag 120
 QY 121 CAGACGACGAGATCACTCCAGATCACTGCACTCCAGATCACTGAG 180
 DB 89 -----edlaqlpeylaktskyltdeyestgctgtcl 120
 QY 181 MKAVLNKQGVNACILPILQIDRDSGNPQVLVNAQCTDYYRGHSALHAIERKSLQCVK 240
 DB 121 mkavlnkqgvnaciilplldrdsqnpqlvnaqctdyyrghsalhatelerslqcvk 180
 QY 241 LIVENGANVBARACGREFGOGCEFEGLPILSIACQWQVSVLLNPNQAPASLOA 300
 DB 181 livenganvbaracgrfegogcefeqlpilsiactqvwvsvllnnpnqapa180 240
 QY 301 TDSOGNTVLHALVMSIDNSAENIALVTSMDGLQAGARLCPVQLEDIRNLQDLTPKL 360
 DB 241 tdsogntvlhalvmsidsaenialvtsmdgllqagarlcpvqledirnlqdltpkl 300
 QY 361 AAREGKREIRHILQREFSLSHSRFTWCWCGPRAVSLYDASVDSCEVSELTIAF 420
 DB 301 aaregkreirhiltrefslshsrftwcwcpvraslydasvdsceensvleltiaf 360
 QY 421 HCKSPHHRVLEPLNKLQAKMDLIPKEFINFLCNLYNFIPTAVAHOPTLKQOA 480
 DB 361 hcksphrvleplnklqakmdlipkefinflcnlynfiftavahopltlkqoa 420
 QY 481 PHKAEVGNMILTGHLILGSIYLLVQGLWFWRRHVEIWSFIDSYEIEFLFOAL 540
 DB 421 phkaevgnmiltghlilgsiyllvqglwfwrrhveiwsfidsyieflfgoal 480
 QY 541 TVVSOVCELAIRMYLPLVLSALVGLMNLVYTRGFQHRGITSVNIQKYLIDLRLFL 600
 DB 481 tvvsovceclairmylplvlsalvglmnlvyrtrgfqhrgitvniqkylidlrlfl 540
 QY 601 IYLVLEGEFVALVLSQEAARPEAPTGPNATESVOPMEQDEGNGAORGLTEASLEL 660
 DB 541 iylvlegefvalvlsqeaarpeaptgpnatesvopmeqdegnagayrglileaslel 600
 QY 661 FKRTTGKELAFODQLHFRGMVLLLLIAYVLLTYILLNLNLALMSETVNSVATDSMSIW 720
 DB 601 fkrttgkelafoqlhfrgmvllyllayvlltyillnmlalmaetvnsavtdsawslw 660
 QY 721 KLGKALSVLEMENGYMWRKROKORAGVNLVYGTCTPDGSPDERMCFRVEVWMAWEDTLPI 780
 DB 661 klgkalsvlemengymwrkrokoragvnlvylgtctpdgspdermcfrrvevwmawedtlpi 720
 QY 781 LCEDPSGAGVPTLENPVLASPKEDDGASEENYVPVOLQSN 824
 DB 781 lc edpsgagvptlenpvlaspkeddgaseenyvpvolqsn 824

DB 721 lcedpsgagvptlenpvlaspkeddgaseenyvpvolqsn 764
 RESULT 2
 AAY06559
 ID AAY06559 standard; Protein; 764 AA.
 XX
 AC AAY06559;
 XX
 DT 08-OCT-1999 (first entry)
 XX
 DE Human vanilloid receptor-related polypeptide 1 (VRP-1).
 XX
 KW Vanilloid receptor-related polypeptide 1; VRP-1; VR2;
 KW capsaicin receptor; VR1; human; vanilloid; analgesic; pain;
 KW inflammation; therapy; diagnosis.
 XX
 OS Homo sapiens.
 XX
 PN WO937675-A1.
 XX
 PD 29-JUL-1999.
 XX
 PF 22-JAN-1999; 99MO-US01418.
 XX
 PR 22-JAN-1998; 98US-0072151.
 XX
 PA (REGC) UNIV CALIFORNIA.
 XX
 PI Brake AJ, Caterina M, Julius DJ;
 XX
 DR WPI; 1999-469113/39.
 DR N-PSDB; AAX87492.
 XX
 PT New isolated capsaicin receptor polypeptide and related nucleic acid
 PT - useful for detecting vanilloid compounds, identifying modulators,
 PT and in diagnosis or treatment of e.g. pain and inflammation
 XX
 XX Claim 4; Page 110-112; 120pp; English.
 PS
 CC The present sequence represents human vanilloid receptor-related
 CC polypeptide 1 (VRP-1 or VR2), as deduced from a cDNA clone (see
 CC AAX87492) isolated from human CCRF-CEM cells. VRP-1 is an
 CC example of a capsaicin receptor-related polypeptide of the
 CC invention. It is not activated by capsaicin or heat, but may
 CC interact with the novel capsaicin receptor VR1 (see AAY06558). The
 CC invention provides vanilloid receptor polypeptides and
 CC polynucleotides, including capsaicin receptor-related polypeptides
 CC and polynucleotides, as well as expression vectors, host cells and
 CC transgenic animals. It also provides a method of using such
 CC receptors to identify vanilloid compounds in natural products or
 CC to screen candidate compounds that modulate capsaicin receptor
 CC function for use as analgesics (vanilloid analogues, therapeutic
 CC antibodies, antisense oligonucleotides, capsaicin receptor-encoding
 CC polynucleotides for gene therapy), flavour-enhancing agents, etc.
 CC Capsaicin receptor-related polypeptides and specific antibodies can
 CC also be used for the diagnosis and treatment of human disease and
 CC pain.
 XX
 XX Sequence 764 AA:
 SO
 Query Match 90.6%; Score 3964; DB 20; Length 764;
 Best Local Similarity 92.7%; Pred. No. 0;
 Matches 764; Conservative 0; Mismatches 0; Indels 60; Gaps 1;
 QY 1 MTSFSSSPVRLERLDDGGEDSGADRGKIDFGSGLPMSQOGEDEKRAPIRVNLNY 60
 DB 1 mtspspsvrlrletldgggedsgadrgkldfgsglpmsqfgedrktapqrlrvnlly 60
 QY 61 RKGTGASQDPNFRDRLFNAYSRGVPGAGATCTGGCTGCACTCCAGATCACTGAG 120
 DB 61 rkgtgasqdpnfrdrlfnaysrgvpgagatctggctgcactccagatcactgag 120
 DB 61 rkgtgasqdpnfrdrlfnaysrgv----- 88

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OY 121 CAMAGCAGCAAGTACTACCGACGCGEDLAGLPEYLSKTSKYLTDSEYTGKTKCL 180
DB 89 -----edlagipeylsktskyltdseytgcgtctcl 120
OY 181 MKAVLNKLDGVNACILPLDIDRDSGNPOPLVNNOCITDDYRRGSAHIAIEKSLDQCVK 240
DB 121 MKAVLNKLDGVNACILPLDIDRDSGNPQPLVNAQCDDYRRGSAHIAIEKSLQCVK 180
OY 241 LIVENGANVBARACGRFFGCGTCFFYGELPLSLAECTQMDVSYLLENPHOPASLOA 300
DB 181 livenGANVBARCGRFFGCGTCFFYGELPLSLAECTQMDVSYLLENPHOPASLOA 240
OY 301 TDSQGNVTHALVWISDNASENIALVTSMYDGLIQAQARLCPTVQLEDIRNLQDLPLKLT 360
DB 241 tdsqgnvthAlvMISdNsEnIAlvTSMYdGLIqAqARlCpTvQlEdIRnLqdlPlKl 300
OY 361 AAEGKIEIFRHLQREFGSLSLSRKFTWCYGPVAVSIXDASVDSCEENSVLEITAF 420
DB 301 aAegKIElFRhLQrEfGslSlSrKfTWcYgPvAvSiXdASvDSCEeNSvLEITAf 360
OY 421 HCKSPRRHRMNVLEPLNKLQAKMDLIPKFFLNFCNLTYMFFTPAVAYHOPTLKKQAA 480
DB 361 hckSPrrHrmvLEplnKlQakMDlIPkFFlNfCnlTYmFFtPAvAYhOPTlKkQAA 420
OY 481 PHIKAEVGNMSMLTGHILLLGSIYLVGOLWYFRRHVFIMISFIDSYPEILFLFOALL 540
DB 421 phIkAeVgNsMlLTghIlLLGsiYlVgOLwYfRRHvFIMISfIDSYpEILfLFoALL 480
OY 541 TVVSVQLCLATFMYPLVLSAVLGNMLLYTRGFORHGTISVMIQKYLIDDLRFL 600
DB 481 tvvSVqlCLATfMYpLVLSaVLGNmLLYtRGfORhGTISvMIQkYLIDDLrFL 540
OY 601 IYLVLEFGAVALVLSQBARPEAPTPGNATSVQPMEGDEGNGAQRGILTEASLEL 660
DB 541 IyLVlEfgAvaLVLSqBARpEAPtPGNATsVQPMegDEgNGAQRGIlTEASlEL 600
OY 661 EKFPTTGMGELAFQEOULHFRGMVLLLLAYVLLTYILLNKLALMSETVNSVATDSMSIW 720
DB 601 eKfPtTgmGElAfQEOuLhFRGMvLLlLLAYvLLTYIlLLnKLAlMSEtVNSvATDSMSIW 660
OY 721 KLOKASVLEMGNGYWKCKKORAGVNLTVGRPDGSPDERKCFRVEYVMASWEOITLP 780
DB 661 kLoKASvLEmgNgYwKcKkORAGvNLtVGRpDGSPDERKcFRVEYvMASwEOITLP 720
OY 781 LCEDPGAGVPRTLENPVLASPPKEDEGASSENVYVOLLQSN 824
DB 721 lceDPgagVpRTlENpVLASpPKedEdgASeENVyVOLLqSN 764

RESULT 3
AA97358
ID AA97358 standard; Protein; 764 AA.
AC AA97358;
XX
XX 05-SEP-2000 (first entry)
DE Human VR-2 protein.
XX
XX VR-2; human; vanilloid receptor; nociceptor; pain signalling;
KM hyperalgesia; musculoskeletal disorder; neuropathic pain;
KM chromosome 17p11-12; gene therapy.
OS
XX Homo sapiens.
PH Key Location/Qualifiers
FT Modified-site 2..5
FT /note= "CGMP-dependent protein kinase
FT phosphorylation site"
FT Domain 162..194
FT /label= ankyrin_repeat_domain
FT Modified-site 169..174

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FT Modified-site 171..174
FT /note= "N-glycosylation site"
FT Modified-site 192..195
FT /note= "N-glycosylation site"
FT Domain 208..243
FT /label= ankyrin_repeat_domain
FT Domain 293..328
FT /label= ankyrin_repeat_domain
FT Modified-site 368..371
FT /note= "CGMP-dependent protein kinase
FT phosphorylation site"
FT Modified-site 368..375
FT /note= "tyrosine kinase phosphorylation site"
FT Domain 391..410
FT /label= transmembrane_domain
FT Domain 431..448
FT /label= transmembrane_domain
FT Domain 459..476
FT /label= transmembrane_domain
FT Domain 486..508
FT /label= transmembrane_domain
FT Modified-site 499..502
FT /note= "CGMP-dependent protein kinase
FT phosphorylation site"
FT Domain 538..556
FT /label= transmembrane_domain
FT Modified-site 604..607
FT /note= "N-glycosylation site"
FT Domain 621..645
FT /label= transmembrane_domain
FT Modified-site 622..628
FT /note= "tyrosine kinase phosphorylation site"
FT Modified-site 749..752
FT /note= "N-glycosylation site"
FT Modified-site 765..770
FT /note= "myristoylation site"

MO200029577-A1.
25-MAY-2000.
12-NOV-1999; 99WO-US26701.
13-NOV-1998; 98US-0108322.
PR 28-DEC-1998; 98US-0114078.
PR 26-FEB-1999; 99US-0258633.
PR 19-OCT-1999; 99US-0421134.
(MILL-) MILLENNIUM PHARM INC.
Curtis RAJ.
WPI: 2000-387790/33.
DR N-PSDB: AAA30254.
PS New capsacin/vanilloid receptor polynucleotides and polypeptides, used
XX to modulate pain signalling mechanisms
XX
XX Claim 11; Fig 2; 183pp; English.

The present sequence is the protein sequence for human
capsacin/vanilloid receptor VR-2, which is involved in pain signalling.
The coding sequence was isolated by searching a heart cDNA library for
genes encoding novel receptors of the capsacin/vanilloid family, and has
been shown to be located at chromosome 17p11-12. This region has been
associated with myasthenia gravis, Smith-Magenis syndrome, COR5,
CC cone-rod dystrophy, choroidal dystrophy, central areolar and retinal cone
CC dystrophy, and it is possible that the protein may be used to treat or
CC diagnose these disorders. In addition, the gene, protein and its
CC antibodies can be used to diagnose and treat hyperalgesia, inflammation,
CC infection, ischaemia, joint pain, tooth pain, headaches, pain associated
CC with surgery or neuropathic pain, possibly via the use of gene therapy.

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XX Sequence 764 AA;

Query Match 90.6%; Score 3964; DB 21; Length 764;
Best Local Similarity 92.7%; Pred. No. 0;
Matches 764; Conservative 0; Mismatches 0; Indels 60; Gaps 1;

```

QY 1 MTPSSSPVFLRLTLDGQEDSGSEADRGKLDGSGLPMPESQFOGEDRKFPAPQIRVNLNY 60
DB 1 mtpssspvflrltldgqedsgeadrgklidgsglpmpesqfgedrkfpapqirvnl 60
QY 61 RKGTASQPDNRPDRDLFNAVSRGVPAGAGATCTGGCTGACTCCAGAGTACCTGAG 120
DB 61 rkgtasqpdnrfdrdlfnavsrgrp-----edlaglpeylsktskyltdseyegstgkcl 88
QY 121 CAAGACGACGACGACTCCAGACTGEDIAGLPEYLSKTSKYLTDSEYEGSTGKTCL 180
DB 89 -----edlaglpeylsktskyltdseyegstgkcl 120
QY 181 MKAVLNKDGYNACILPLQLQIDRDGSGNPQPLVNAQCTDDYRGRSALHIAIEKRSIQCVK 240
DB 121 mkavlnldgynacilplqlqidsrsgnpplvnagctddyrrghsalhialekrsiqcvk 180
QY 241 LIVENGANVHARACGRFFQKGCCTCFYRGELPLSLAACKQMDVSYLLENPHQASIQQA 300
DB 181 livenganvharcgrffqkgctcfyrgelplslactkqmdvsvyllenphqasiqqa 240
QY 301 TDSQGNVTLHALVMTSDNSAENIALVMTSDGLQAGARLCPYQLDIRMLDLPKL 360
DB 241 tdsqgnvlnhalvmtsdnsaenialvmtsgdlqagartcpvqldirmlldlpkl 300
QY 361 AAREGKIEFRHILQREFSGLSHRKFTENCYGPVRSYLDLASVDSCEENSVLEITIAF 420
DB 301 aaregkiefrhilqrefsglsshrktencygpvrsvlyldasvdsceensvleitiaf 360
QY 421 HCKSPHRRHNVLEPRLNKLQAKMDLIPKFFLNFLCNLIYMFIFTAVANHQPLKKQAA 480
DB 361 hcksphrhnmvleprlnklqakmdlipkfflnflcnliymfiftavanhqplkkqaa 420
QY 481 PHLKAENGSMLTGHILILGGIYILVGOIMFWRHVFIMISFIDSYFEILFEQL 540
DB 421 phlkaevngsmlltghililggiiylvgolmfwrrhvfimisfidisyfeilfeql 480
QY 541 TVVSOVLCFLAIEWYLPFLVSAVLGWMNLNLTXTRGQHTGYSVMIOKVLIRDLRPL 600
DB 481 tvsqvclcfllawylpflvsalvgwmnlntxtrgqhtgysvmiokvllrdlrpl 540
QY 601 IYLVPLREFAVALYSLSGEARRPAPPGPNATSEVQPMEGEDSGNAGQVIGILEASIEL 660
DB 541 iylvplrfavalyslsgearrpaprpnatesevqpmegedsgnagqvigileasiel 600
QY 661 FKFTIGMELAFQOLHFRGAVLLLLAYLVLLFTYLLNMLIALMSETVNVSATDSMSIW 720
DB 601 fkftigmelafqolhfrgavllllaylvllftyllnmlialmsetvnvsatdsmsiw 660
QY 721 KLOKAISTYLENENGYWCKRKQKQAGVMTYGTGKPDGSPDERMCFRVEEVNMAWEOQLPT 780
DB 661 klqkaistylenengywckrkqkqagvmtlygtgkpdgspdermcfreveevnmawegqlpt 720
QY 781 LCEPSSGAGVPRTLNPPLASPPKEDDGAASEENYVVPOLLQSN 824
DB 721 lcepsgagvprtlnpplaspkdedgaaseenyvvpollqsn 764

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RESULT 4
AAB35622
ID AAB35622 standard; Protein; 764 AA.

XX AAB35622;
XX 14-FEB-2001 (first entry)
XX

DE Human vanilloid receptor like receptor protein.
XX
XX VR-L; vanilloid receptor-like receptor; pain; infection; allergy;
KW mechanical injury; lymphoid tissue; human.
XX
XX Homo sapiens.
OS
XX GB2346882-A.
FN
XX 23-AUG-2000.
PD
XX
XX 02-DEC-1999; 99GB-0028566.
PE
XX
XX 08-DEC-1998; 98GB-0027016.
PR
XX
XX (MERI) MERCK SHARP & DOHME LTD.
PA
XX
XX Bonnett TP;
PI
XX
XX WPI: 2001-064250/08.
DR
XX N-PSDB: AAC60297.
NR
XX

PT New polynucleotide encoding human vanilloid receptor-like receptor for
PT diagnosing and treating pain, infections, allergies, and cancers
XX
XX Claim 1; Fig 1; 36pp; English.

CC The present invention relates to the human vanilloid receptor-like
CC receptor. This receptor may be used for diagnosing or treating
CC conditions associated with altered vanilloid receptor-like (VR-L)
CC receptor expression. It may also be used to treat abnormal conditions
CC associated with pain. Conditions or diseases that can be diagnosed or
CC treated include viral, bacterial and fungal infections, allergic
CC responses, mechanical injury associated with trauma, hereditary
CC diseases, lymphoma or carcinoma, or other conditions which activate
CC the genes of the lymphoid tissues.
XX
XX

Sequence 764 AA;

Query Match 90.6%; Score 3964; DB 22; Length 764;
Best Local Similarity 92.7%; Pred. No. 0;
Matches 764; Conservative 0; Mismatches 0; Indels 60; Gaps 1;

```

QY 1 MTPSSSPVFLRLTLDGQEDSGSEADRGKLDGSGLPMPESQFOGEDRKFPAPQIRVNLNY 60
DB 1 mtpssspvflrltldgqedsgeadrgklidgsglpmpesqfgedrkfpapqirvnl 60
QY 61 RKGTASQPDNRPDRDLFNAVSRGVPAGAGATCTGGCTGACTCCAGAGTACCTGAG 120
DB 61 rkgtasqpdnrfdrdlfnavsrgrp-----edlaglpeylsktskyltdseyegstgkcl 88
QY 121 CAAGACGACGACGACTCCAGACTGEDIAGLPEYLSKTSKYLTDSEYEGSTGKTCL 180
DB 89 -----edlaglpeylsktskyltdseyegstgkcl 120
QY 181 MKAVLNKDGYNACILPLQLQIDRDGSGNPQPLVNAQCTDDYRGRSALHIAIEKRSIQCVK 240
DB 121 mkavlnldgynacilplqlqidsrsgnpplvnagctddyrrghsalhialekrsiqcvk 180
QY 241 LIVENGANVHARACGRFFQKGCCTCFYRGELPLSLAACKQMDVSYLLENPHQASIQQA 300
DB 181 livenganvharcgrffqkgctcfyrgelplslactkqmdvsvyllenphqasiqqa 240
QY 301 TDSQGNVTLHALVMTSDNSAENIALVMTSDGLQAGARLCPYQLDIRMLDLPKL 360
DB 241 tdsqgnvlnhalvmtsdnsaenialvmtsgdlqagartcpvqldirmlldlpkl 300
QY 361 AAREGKIEFRHILQREFSGLSHRKFTENCYGPVRSYLDLASVDSCEENSVLEITIAF 420
DB 301 aaregkiefrhilqrefsglsshrktencygpvrsvlyldasvdsceensvleitiaf 360
QY 421 HCKSPHRRHNVLEPRLNKLQAKMDLIPKFFLNFLCNLIYMFIFTAVANHQPLKKQAA 480

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Db 361 hckspnrhmwvlepnlkllgkwdlllpkfflnfclnllymffitavayhgpclkkqaa 420
Oy 481 PHLKAEGNSMLTGHILLGLGIYLVGOLWYFMRHVFMTISFIDSFEILFEOALL 540
Db 421 phlkaevgsmltghlllllgyllyvgqlwyfwrhvfivsfidsyfeillfifgall 480
Oy 541 TVVSOVLCFLAEMWLPPLVSALVGLWMLLYTRGFORTGTVSVIOWXVILRDLRFL 600
Db 481 tvvsgvllcflaewypllvlsalvlgwmllytrgfgortgtyvsmiqvllldlrfl 540
Oy 601 IYLVLEFGFAVLVLSOAMRPEARTGPNATESVOPMGEOEGAGAOYRGILEASTEL 660
Db 541 IYLVLEFGFAVLVLSOAMRPEARTGPNATESVOPMGEOEGAGAOYRGILEASTEL 600
Oy 661 FKFTIGMELAQEOQLHFRGMVLLLLAVLLTYILLNMLIALMSETVNSVATDSWSIW 720
Db 601 kfttgmglatqeqhftgwmvlllllyvlltylllmlalmetvnsvatdswslw 660
Oy 721 KIQKAI SVLEMENGYWCKKQKQAGVMTVGTPDGSPPERMCFRVEEYVNMASMEOTLPT 780
Db 661 kIQKAIsvlemengywckkqkqagvmtvgtpdgsppermcfrveeynmasmeotlpt 720
Oy 781 IGEDPSGAGVPTLENPVLASPKEDGASEBNYVNPOLLQSN 824
Db 721 IGEDPSGAGVPTLENPVLASPKEDGASEBNYVNPOLLQSN 764

RESULT 5
ID AAY42308
AAY42308 standard; Protein; 763 AA.
XX AAY42308;
DT 06-DEC-1999 (first entry)
XX Human vanilloid receptor-like cation channel (hVRCC).
XX Vanilloid; capsaicin; neuron; selective; calcium; cation; receptor; pain;
XX inflammation; brain disease; cancer; autoimmune disorder.
XX Homo sapiens.
XX Key Location/Qualifiers
XX MISC-difference 5 /note- "Optionally Phe in an allelic variant"
XX MISC-difference 417..418 /note- "Optionally there is an insertion of a Gln residue
XX in an allelic variant"
XX MO9946377-A2.
XX 16-SEP-1999.
XX 10-MAR-1999; 99WO-EP01550.
XX 11-MAR-1998; 98EP-0400565.
XX (SNFI ) SANOFI-SYNTHELABO.
XX Partisect M, Renard S;
XX WPI; 1999-571722/48.
XX N-PSDB; AAZ42308.
XX New receptor-like channel polypeptide and polynucleotide useful for
XX prevention and treatment of cancer, autoimmune disease, brain disease
XX and ulcers.
XX Claim 12; Page 15; 50pp; English.
XX This sequence represents a human vanilloid receptor-like cation channel
XX (hVRCC). This channel is activated by vanilloids such as capsaicin

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CC and resiniferatoxin, and is expressed in a variety of tissues,
CC particularly in nervous tissue such as the amygdala, substantia nigra,
CC thalamus, dorsal root ganglia and spinal cord. Vanilloids are natural
CC compounds which are known to trigger cation permeability in the
CC peripheral neurons involved in transmission of noxious stimuli (e.g.,
CC mechanical, chemical or thermal). A recently discovered rat
CC vanilloid-gated cation channel, which is highly expressed in dorsal root
CC ganglia, has six putative transmembrane domains, giving it significant
CC structural homology with "store-operated" calcium channels, and is highly
CC selective for calcium ions. hVRCC and nucleotides encoding it can be used
CC in prevention, diagnosis or therapy of disorders that may be associated
CC with an excess or deficiency of hVRCC. Disorders detected or treated
CC using hVRCC proteins, nucleotides or antagonists include chronic
CC inflammation, acute and chronic pain, brain diseases, abnormal
CC proliferation and cancer, ulcers, autoimmune diseases, control of viscera
CC innervated by the dorsal root ganglia neurons, to mimic or antagonise
CC effect of endogenous neurotransmitters and hormones, and to inhibit graft
CC rejection by promoting immunosuppression. Nucleotide sequences encoding
CC hVRCC are also useful for chromosome localisation.
XX
SQ Sequence 763 AA:
Query Match 90.2%; Score 3948.5; DB 20; Length 763;
Best Local Similarity 92.6%; Pred. No. 0;
Matches 763; Conservative 0; Mismatches 0; Indels 61; Gaps 2;
Oy 1 MTPSSSPVFRLETLGGGEGDSEADRGKIDPSSGIPMSESOPGQDGRFAQIRVNLNY 60
Db 1 mtpssspvfrletldgggedseadrgkldtsgipmnesqfgedrftapqirvnlly 60
Oy 61 RKGTGASQPDNFRDRLFNNAVSRGVPGAGATCGGCTGAGACTCCAGAGACTGAG 120
Db 61 rkgtgasqpdnfrdrlfnnavsrgvpgagatcggtgagactccagagactgag 88
Oy 121 CAAGACCAAGCAAGTACCTGACGACTCGEDLAGLPYLSKTSKYLTDSEYTESGTGTL 180
Db 89 -----edlaglpelylaktskyltdseytesgtgktcl 120
Oy 181 MKAVNLKCGVNACTPLQIDRDSGNPQPLVNAOCTDDIYRGHSLHAIKRSIQCYK 240
Db 121 mkavnlkcgvnacpllqidrdsnpplvnaqctddyyrghslhalekrsiqcyk 180
Oy 241 LVYENGANVHARAGRFQFGGCTCFEGELPLSLACTKQMDVSYLLENPHOPSLQA 300
Db 241 lvenganyharagrfqfggctcfegelpslactkqmdvsysyllenphopslla 300
Oy 301 TDSQNTVLHALVMTSDNSAENIALVTSMYDGLQAGARLCTVVOLEDIRNODLTPKL 360
Db 301 tdsqntvlhalvmtsdnsaenialvtsmydglqagarlcvvledirnodltpkl 360
Oy 361 AAKEGKIEFRHILQRESGLSHLSKRTKTCYGPVRSVLYDLASVDCSENSVLEITAF 420
Db 361 aakegkiefrhilqresglskrtkctcygpvrsvlydlasvdcseensvleiaf 420
Oy 421 HCKSPHRHMVLEPNTKLOAKMOLLKPFNLFLCNLYVFTFAYVHOPTLAKQAA 480
Db 421 hckspnrhmwvlepnlkllgkwdlllpkfflnfclnllymffitavayhgpcllk-aa 419
Oy 361 hckspnrhmwvlepnlkllgkwdlllpkfflnfclnllymffitavayhgpcllk-aa 419
Oy 481 PHLKAEGNSMLTGHILLGLGIYLVGOLWYFMRHVFMTISFIDSFEILFEOALL 540
Db 420 phlkaevgsmltghlllllgyllyvgqlwyfwrhvfivsfidsyfeillfifgall 479
Oy 541 TVVSOVLCFLAEMWLPPLVSALVGLWMLLYTRGFORTGTVSVIOWXVILRDLRFL 600
Db 480 tvvsgvllcflaewypllvlsalvlgwmllytrgfgortgtyvsmiqvllldlrfl 539
Oy 601 IYLVLEFGFAVLVLSOAMRPEARTGPNATESVOPMGEOEGAGAOYRGILEASTEL 660
Db 540 IYLVLEFGFAVLVLSOAMRPEARTGPNATESVOPMGEOEGAGAOYRGILEASTEL 599
Oy 661 FKFTIGMELAQEOQLHFRGMVLLLLAVLLTYILLNMLIALMSETVNSVATDSWSIW 720

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Db 600 fktlmgelafqeqhfrgmvlilllayvillylllmliamsetvnsvaldsxslw 659
 QY 721 KLOKAISVLEMGNGYWMCKRKORAGVMTLVGTRKPDGSPDERMCFRVEEVNMAWSEQTLP 780
 Db 660 klqkalsvlemengywwcckkqragymltvgckpdspsderwcfvveevnaswecqlpt 719
 QY 781 LCEDPSGAGVPRTLENPVLASPPKEDGASEENYVPVOLLOSN 824
 Db 720 lcebpsgagvprtlempvlasppkeddgaseenyvpyqlqsn 763

RESULT 6

AAV29471
 ID AAV29471 standard; Protein; 763 AA.

AAV29471;

08-OCT-1999 (first entry)

Human vanilloid receptor homologue VANILREP2 polymorphic variant PVP-1.

Human; vanilloid receptor homologue; VANILREP2; polymorphic variant; PVP-1; therapy; diagnosis; chronic pain; neuropathic; postoperative; rheumatoid arthritis; neuralgia; algesia; nerve injury; ischaemia; neurodegeneration; stroke; incontinence; inflammatory disorder.

Homio sapiens.

WO9937765-A1.

29-JUL-1999.

25-JAN-1999; 99WO-EP00420.

20-JAN-1999; 99GB-0001209.

27-JAN-1998; 98EP-0300549.

26-OCT-1998; 98GB-0023421.

(SMK) SMITHKLINE BEECHAM PLC.

Davis JB, Duckworth DM, Hayes PD;

WPI: 1999-479049/40.

N-PSDB; AA207116.

New human vanilloid receptor homologues (VANILREP2)

Claim 4; Page 35-37; 47pp; English.

The present sequence represents a human vanilloid receptor homologue VANILREP2 polymorphic variant PVP-1. VANILREP2 can be used to diagnose disease or susceptibility to disease related to expression or activity of VANILREP2 polypeptides. VANILREP2 may be used to treat diseases including pain, (for example chronic, neuropathic, postoperative, rheumatoid arthritis), neuralgia, algesia, nerve injury, ischaemia, neurodegeneration, stroke, incontinence, and inflammatory disorders.

Sequence 763 AA;

Query Match 90.2%; Score 3948.5; DB 20; Length 763;

Best Local Similarity 92.6%; Pred. No. 0;

Matches 763; Conservative 0; Mismatches 0; Indels 61; Gaps 2;

QY 1 MTSPPSPVFRLETLDDGQEDSGEADRGKLDGSGLPMESEFOGEDRRKPAQIVNLTNY 60
 Db 1 mtsppspvfrletlddgqedsgeadrgklidgsglpmeesfggedrktfapqivnltny 60
 QY 61 RKGTASGAPDPNRFDRDLFNNAVSRGVPAGAGATCTGGCTGACTTCAGAGTACCTGAG 120
 Db 61 rkgtasgapdpnrfdrrdlfnnavsrgrp----- 88
 QY 121 CAAGACGACGACGACTCACCAGCTCGEDLAGLPFYLSTKSTKYLTDESYTEGSTGTCTCL 180

Db 89 -----edlaglpeytskstkyltdeytestgtctcl 120
 QY 181 MKAVLNKGVNACILPLQIDRDSGNPOLYNAOCTDDYVGHSAHLAIEKRSLOCK 240
 Db 121 mkavlnkgvnaci|pl|q|drds|gnp|y|na|oc|td|y|v|gh|sa|h|a|ie|k|rs|lo|ck 180
 QY 241 LLVNGANVHARACGRFPOKGGTCFYEGLPLSLAACKTQWDVSYLLENPHOASLOA 300
 Db 181 llvnganvhara|c|g|r|f|p|o|k|g|g|t|c|f|y|e|g|l|p|s|l|a|a|c|k|t|q|w|d|v|s|y|l|e|n|p|h|o|a|s|l|o|a 240
 QY 301 TDSOGNTVHALVMTSDNNAENALVTSMDGLQAGARLCTVQIEDIRNODLTPKL 360
 Db 241 tdsogn|t|v|h|a|l|v|m|t|s|d|n|n|a|e|n|a|l|v|t|s|m|d|g|l|q|a|g|a|r|l|c|t|v|q|i|e|d|i|r|n|o|d|l|t|p|k|l 300
 QY 361 AAKEKIEIFRHILOREFSGLSHLSKRFEMCYGPVRYLYOLASVDSCEENSVLEIIF 420
 Db 301 aa|e|k|ie|i|f|r|h|i|l|o|r|e|f|s|g|l|s|h|l|s|k|r|f|e|m|c|y|g|p|v|r|y|l|y|o|l|a|s|v|d|s|c|e|e|n|s|v|l|e|i|i|f 360
 QY 421 HCKSPHRHRMVLEPLNKLQAKMDLLPRFLNLCNLIYMFITAVAYHOPTRKQAA 480
 Db 361 hcksp|hr|hr|m|v|l|e|p|l|n|k|l|q|a|k|w|d|l|l|p|r|f|l|n|l|c|n|l|i|y|m|f|i|t|a|v|a|y|h|o|p|t|r|k|q|a|a 419
 QY 481 PHLKAEVGNMILTGHIILLOGITLVGQLWTFMRHRVFTISFIDSIFELPLFOALL 540
 Db 420 phl|k|a|e|v|g|n|m|i|l|t|g|h|i|i|l|l|o|g|i|t|l|v|g|q|l|w|t|f|m|r|h|r|v|f|t|i|s|f|i|d|i|s|i|f|e|l|p|l|f|o|a|l|l 479
 QY 541 TVVSQVLCFLAIEWYLPILVSALVAGMLNLKYTGSEFOTGYSVWICKVITRDLRFL 600
 Db 480 tv|s|q|v|l|c|f|l|a|i|e|w|y|l|p|i|l|v|s|a|l|v|a|g|m|l|n|l|k|y|t|g|s|e|f|o|t|g|y|s|v|w|i|c|k|v|i|t|r|d|l|r|f|l 539
 QY 601 IYLVFEGFAVALVSLGSEAMRPEAPGPNATESVOPMEGDEGNGAQRILEASLEL 660
 Db 540 i|y|l|v|f|e|g|f|a|v|a|l|v|s|l|g|s|e|a|m|r|p|e|a|p|g|p|n|a|t|e|s|v|o|p|m|e|g|d|e|g|n|g|a|q|r|i|l|e|a|s|l|e|l 599
 QY 661 EKFTTGMEFLAQEOLHRGMVLLLLAYVLTITLLNMLALMSEYNSVATDSWSIW 720
 Db 600 e|k|f|t|t|g|m|e|f|l|a|q|e|o|l|h|r|g|m|v|l|l|l|l|a|y|v|l|t|i|t|l|l|n|m|l|a|m|s|e|y|n|s|v|a|t|d|s|w|i|w 659
 QY 721 KLOKAISVLEMGNGYWMCKRKORAGVMTLVGTRKPDGSPDERMCFRVEEVNMAWSEQTLP 780
 Db 660 klqkalsvlemengywwcckkqragymltvgckpdspsderwcfvveevnaswecqlpt 719
 QY 781 LCEDPSGAGVPRTLENPVLASPPKEDGASEENYVPVOLLOSN 824
 Db 720 lcebpsgagvprtlempvlasppkeddgaseenyvpyqlqsn 763

RESULT 7

AAV84834
 ID AAV84834 standard; Protein; 764 AA.

AAV84834;

08-AUG-2000 (first entry)

Amino acid sequence of a vanilloid receptor-like (VR-L) protein.

Cation channel protein; vanilloid receptor-like 1 protein; VR-L; noxious heat; pain; inflammation; tissue damage; nociception; gene therapy; sensory neuron; immune system; analgesic; immunomodulatory; neuromodulatory.

Homo sapiens.

Key Location/Qualifiers

Misc-difference 149 /note= "Gly encoded by CAG"

Region. /note= "ankyrin-like repeat"

Misc-difference 200 /note= "Lys encoded by AAT"

Region 208..240

[illegible]

QY	121	CAAGACGACGAAGTACCTCACCAGACTCCEDDAGLAGEPEYLSKTSKYLTDSEYEGSTGTCL	180
Db	89	-----edlaqlpeylsktskyltdseytegstgtkcl	120
QY	181	MRAVLNKLKDVNACILPLQLDIDRDSGNPQPLVMAQCTDYVRGSALHAIAREKSLQV	240
Db	121	mkavlnklkgvnaclllpqlldtidsngpplvnaqctdyvrghsalhaiekslqcvk	180
QY	241	LIVENANVHAARACGRFPOKGGCTGTFYGEPLSLAIACTKQMDVVSYLENPHQASLQA	300
Db	181	llvengaanvharaqgrffqkggctcfyfgelplslactkqmdvvsyllenphqaslqa	240
QY	301	TDSOGTFVHALVMTSDNSAENIALVSMYQGLQAGAKRLCPYQLEDIRNLQDLPTPLK	360
Db	241	tdsogtfvhalvmtsdnsaenialvsmyqglqagarklcpvtqledirnlqdlptplk	300
QY	361	AAKEGKIEIFRHIIIDREFSGLSHLRSKRTKTEWCYGVRSYLDLASVSCSENSYLEIAF	420
Db	301	aakegkiefrrhiiidrefsglsghlrsrktketcypvrsyldlasvdsceensyleiaf	360
QY	421	HCKSPHRBMVLEPLNKLQAKWDLIPKEFLNFCNLIMYETFTAVAYHQPLKROAA	480
Db	361	hcksphrbmvlleplnklqakwdlppkefflnfcnlmyetftavayhqplrkqaa	420
QY	481	PHLKAEVNGSMILTGHIILILAGGTYLVGLQMTFRRRHVFIMWIFDSYFELIFLQAL	540
Db	421	phlkaevgnsmltghiiililaggtylvglqmtfrrrhvfimwifdsyfeliflqal	480
QY	541	TIVSOVLCEFLAIEMVLPPLVSALVYGMNLTYTRGPHGTYSVMIOXVILDBLPELL	600
Db	481	tivsylvclflvemylpplvsalvymnltytrgphgtysvmioxvildblpell	540
QY	601	IYLVFLFGRFAVALVLSQGANRPEAPTEGPNATSEVQPMEGDEGNAQYRGILIASLEL	660
Db	541	ilyvlflfgrfavalvlsqganrpeaptegnatsevpmegegdegnagrygileaslel	600
QY	661	KFTFTGMELAFQEDLHNRGAVLLLLLAVYLTYILLNLMIALMSTVNSVATDSKSTW	720
Db	601	kftftgmelaifqedlhnrgravlllllavyltyillnlmialmstvnsvatdskstw	660
QY	721	KLOKAIISYLEMENGYYMCCRKORAGVMLTVGTRKPDGSPDERMCFRYEVMWMSQETLPT	780
Db	661	klqkaiixylemenyywccrkkqrgavmltvgtkpdgsperdermcfryevmwmsqetlpt	720
QY	781	LCEDPSGAGVPRLENPYLASPREDEBDGASEENYVVPQLQSN 824	
Db	721	lcedpsgagvprtlempylaspredebdgaseenyvvpqlqsn 764	
RESULT 8			
AA197364			
ID	AA197364	standard; Protein; 630 AA.	
XX	AA197364;		
XX	14-SEP-2000	(first entry)	
XX	Human VR-2 (alternate form) protein.		
KW	VR-2; human; varilliole receptor; nociceptor; pain signalling;		
KM	hyperalgesia; musculoskeletal disorder; neuropathic pain;		
KV	chromosome 17p11-12; gene therapy.		
XX	Homo sapiens.		
OS	MO200029577-A1.		
XX	25-MAY-2000.		
XX	12-NOV-1999;	99MO-05267.01.	
PR	13-NOV-1998;	98US-0108322.	

PR 28-DEC-1998: 98US-0114078.
PR 26-FEB-1999: 98US-0258633.
PR 19-OCT-1999: 99US-0421134.

XX (MILL-) MILLENNIUM PHARM INC.

PA

PI Curtis RAJ;

DR WPI: 2000-387790/33.

XX N-PSDB: AAA30255.

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Sequence 630 AA;

The present sequence is the protein sequence for an alternate form of human capsaicin/vanilloid receptor VR-2, which is involved in pain signalling. The coding sequence was isolated by searching a heart cDNA library for genes encoding novel receptors of the capsaicin/vanilloid family, and has been shown to be located at chromosome 1p11-12. This region has been associated with myasthenia gravis, Smith-Magenis syndrome, CORDS, Cone-rod dystrophy, choroidal dystrophy, central areolar and retinal cone dystrophy, and it is possible that the protein may be used to treat or diagnose these disorders. In addition, the gene, protein and its antibodies can be used to diagnose and treat hyperalgesia, inflammation, infection, ischemia, joint pain, tooth pain, headaches, pain associated with surgery or neuropathic pain, possibly via the use of gene therapy.

Query Match 73.5%; Score 3218; DB 21; Length 630;
Best Local Similarity 76.5%; Pred. No. 7.9e-272;
Matches 630; Conservative 0; Mismatches 0; Indels 194; Gaps 2;

QY 1 MTPSSSSVFRLETLDDGQEDSGEADRKLDPSGLPMEOSFOCEDKRFAPQIVNINLY 60
DB 1 mtpssspvfrletldgqeqdsgedrkldtgsqglpmeqfgedkrfapqlivniny 60
QY 61 RKGTGASOPDPFRFDRDLFNVAWSRGVAGAGATCTGCTGAGACTCCAGACTACTAG 120
DB 61 rkgtgasopdpfrfdrdlfnvaWSRGVAGAGATCTGCTGAGACTCCAGACTACTAG 120
QY 121 CAAGACGACAGACTACTCACCAGACTCGEDLAGLPEYLSTSKYLTDESEYEGSTGKTCL 180
DB 89 -----edlaglpeylstskyltdeyegstgktcl 120
QY 181 MKAVINLMDGVNACLPLQLDIDRDSGNQPLVNAOCTDDYRGHSALHAIKESLQCVK 240
DB 121 mkavinlmdgvnACLPLQLDIDRDSGNQPLVNAOCTDDYRGHSALHAIKESLQCVK 180
QY 241 LLVENGANVHARACGRFQKOGCFYRGELPLSLAACKTMDVSVYLEMHPQASAO 300
DB 241 llvengANVHARACGRFQKOGCFYRGELPLSLAACKTMDVSVYLEMHPQASAO 180
QY 301 TDSOGNTVLAHALVMSIDNSAENIALVSMYDGLQAGARLCPTVOLEDIRMLQDLPKL 360
DB 301 tdsogntvLAHALVMSIDNSAENIALVSMYDGLQAGARLCPTVOLEDIRMLQDLPKL 360
QY 361 AAKGKTIFFHNLIORESGSHSRKTEMCYGPVRSYLDLASVDSCEANSVLEITAF 420
DB 361 aakgkTIFFHNLIORESGSHSRKTEMCYGPVRSYLDLASVDSCEANSVLEITAF 420
QY 421 HCKSPHRRATVLEPLNLLQAKMDLIPKFLNPLCNLYMFTFTAVAYOPLTKQAA 480
DB 421 hckspHRRATVLEPLNLLQAKMDLIPKFLNPLCNLYMFTFTAVAYOPLTKQAA 480
QY 481 PHLAENVGNSMLTGHILILLGGITLLVQGLMFWRRHVFVWISFIDSYEILFLFQALL 540
DB 481 phlaENVGNSMLTGHILILLGGITLLVQGLMFWRRHVFVWISFIDSYEILFLFQALL 540
QY 541 TVSOYLCFLAIEWTLPLLVSAVLGWMNLVYTRNGFQHTGIVSYMIQKVLIDLLRELL 600
DB 541 tvsoyLCFLAIEWTLPLLVSAVLGWMNLVYTRNGFQHTGIVSYMIQKVLIDLLRELL 600
QY 601 IYLVLFQFAVALVLSQEAAMRPEARTGNATSEYQPMHGEDEGNAGVRLSELEL 660
DB 601 iylvLFQFAVALVLSQEAAMRPEARTGNATSEYQPMHGEDEGNAGVRLSELEL 660
QY 661 FKFTIGMELAFQEOLEHFRGNVLLLLAVLLTYILLNMLIALMSETVNSVATDSWSIM 720
DB 661 fkftIGMELAFQEOLEHFRGNVLLLLAVLLTYILLNMLIALMSETVNSVATDSWSIM 720
QY 721 KLOKAISYLENENGITWCKRKORAGVMTLVGTRPGSDPERWCFRVEEVNMAWSEQLTPT 780
DB 721 klokaISYLENENGITWCKRKORAGVMTLVGTRPGSDPERWCFRVEEVNMAWSEQLTPT 780
QY 781 LCEDESGAGVPTLENPVLASPKDEGASRENVVPOLOSN 824
DB 781 lcepsgagvptlenpvlasPKDEGASRENVVPOLOSN 824
QY 824 LCEDESGAGVPTLENPVLASPKDEGASRENVVPOLOSN 824
DB 824 lcepsgagvptlenpvlasPKDEGASRENVVPOLOSN 824

RESULT 9
ID AAY06556 standard; Protein: 761 AA.
AC AAY06556;
DT 08-OCT-1999 (first entry)
DE Rat vanilloid receptor-related polypeptide 1 (VRP-1).
KW Vanilloid receptor-related polypeptide 1; VRP-1; VR2;
KW capsaicin receptor; VR1; rat; vanilloid; analgesic; pain;
KW inflammation; therapy; diagnosis.
OS Rattus rattus.
PN MO9937675-A1.
PD 29-JUL-1999.
PE 22-JAN-1999; 99WO-US01418.
PR 22-JAN-1998; 98US-0072151.
PA (REGC) UNIV CALIFORNIA.
PI Brake AJ, Caterina M, Julius DJ;
DR WPI: 1999-469113/39.
XX N-PSDB: AAX87478.
PT New isolated capsaicin receptor polypeptide and related nucleic acid
PT useful for detecting vanilloid compounds, identifying modulators,
PT and in diagnosis or treatment of e.g. pain and inflammation
PS Claim 4; Page 81-83; 120pp; English.
XX
XX The present sequence represents rat vanilloid receptor-related
XX polypeptide 1 (VRP-1 or VR2), as deduced from a cDNA clone (see
XX AAX87478) isolated from a rat brain cDNA library. VRP-1 is an
XX example of a capsaicin receptor-related polypeptide of the
XX invention. It is not activated by capsaicin or heat, but may
XX interact with the novel capsaicin receptor VR1 (see AAY06555). It
XX shows 49% identity with rat VR1. The invention provides vanilloid
XX receptor polypeptides and polynucleotides, including capsaicin
XX receptor-related polypeptides and polynucleotides, as well as
XX expression vectors, host cells and transgenic animals. It also
XX provides a method of using such receptors to identify vanilloid
XX compounds in natural products or to screen candidate compounds that
XX modulate capsaicin receptor function for use as analgesics (vanilloid
XX analogues, therapeutic antibodies, antisense oligonucleotides,
XX capsaicin receptor-encoding polynucleotides for gene therapy).

CC flavour-enhancing agents, etc. Capsaicin receptor-related
 CC polypeptides and specific antibodies can also be used for the
 CC diagnosis and treatment of human disease and pain.

Sequence 761 AA;

Query Match 68.8%; Score 3011.5; DB 20; Length 761;
 Best Local Similarity 72.0%; Pred. No. 1e-253;
 Matches 598; Conservative 62; Mismatches 93; Indels 77; Gaps 8;

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QY 1 MTSSSSPVRLFTLDGGDEGSEADRGKIDFGSGLPMPESQFGEDKKFAPQIRVNLY 60
DB 1 mtaasspparlrleldsgdeegnaevnkykge-----ppmespfqredrnspqikvnlntf 56
QY 61 -----RKGTGA-SQDPNPRFDRDLFNVAWSRGVPAGAGATCTGCTGACTCCAGAGTAC 115
DB 57 lkrpkrtsapsqgeprfdtrdrfsvvsrgvp----- 89
QY 116 CTGAGCAAGACGACCAAGTACTCACCAGCTCGEDLAGLPEYLSKTSKYLTDSEYEGST 175
DB 90 -----eeltgllleylrwnskyltdsaytegst 116
QY 176 GKTCIMKAVLNKDGYNACTLPLOIDRDGSGNPQPLVNAOCTDYYRGSALHIAIEKRS 235
DB 117 gktclmkavlnldqgyvacimpilqldkdsnpkplvnaqctdefygshahialekrs 176
QY 236 LQCVKLLVENGANVHARACGRFQKGQCTFYFGEPLPLSLAACKQMDVYSLLENPHOP 295
DB 177 lqcvklvengadhlacgrffqkngctcfyfgeplslsackqmdvvylylennph 236
QY 296 ASLQATDSQGNVYVLAHVMISDMSAENIALVTSMYDGLLAGARLCEPTOLEDIRNLQDL 355
DB 237 asleatdsqgnvylahvmisadnsenalvlnmydglqmgarlcptqvgeelsnqgl 296
QY 356 TPKLAKKEKIEFFRIILOREPSG-LSHSKRTEWCYGPVRSVLDAVSCENSV 414
DB 297 tprklakekietfrrilidrepsgpyrslrftewcygpvrsvlydlsavswekns 356
QY 415 LEIATFHCKSPHRRMRYVLEPLNKLQAKMDLIPKFLNPLCLVIMETETANAAYHOPT 474
DB 357 leiathckspnhrrmrvleplnklqekmdlprkflnplclvymetfvaayhops 416
QY 475 LKQQAAPHLEAVGNMNLGTHILLGGITLVGOLMYFWRHVFIMISFIDSYPEILF 534
DB 417 ldqqaapskatfgesmlllghlllllgilylllgqlywvrrrlfwmisfmdyefellf 476
QY 535 LFGALLTVVSOVCELAIEWYLPPLVLSALVGLNLLYTRGQHTGYVMIOKVILRD 594
DB 477 lfqalltvvlsqvrlfmetevyldlvislvglvlnllylrrgfhgilysvmldkvilrd 536
QY 595 LRLFLIYVLFEGFAVALVLSQEAAMPAPAPGNATESVQPMEGDEGDEGNGAOYRGIL 654
DB 537 lrlfllyvlflfgfvalvlsirearspkrpedsnstveqptvgeee--papyrzll 594
QY 655 EASLEEFKRTIGMBELAFQDQLHFGKAVLLILAYVLLYILLNMLIALMSETVSVAT 714
DB 595 easleefkrtigmbelafqeqrlfrgqvllllayvlllyvlllmlialmsetvnhvad 654
QY 715 DSWIRKLKAIIVLEMENGYWMC-RKKORAGVLMYGTDPDGSPPBRWCFFRYEEVWMA 773
DB 655 dswirklkaiivlemengywmcrrtkkhegllkvygtrgdgcpderwtfryeevnmwa 714
QY 774 WEGTLPTECEDPSGAGVPRTELENPVLASPKEDSDASEENVVAVVLOLS 823
DB 715 wegtlpptecepsgagvprtlelenpvlaspkeddsaseenvvavvlylvs 760

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RESULT 10
 AAM99790
 ID AAM99790 standard; Protein; 761 AA.
 AC AAM99790;

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XX 16-JUN-1999 (first entry)
DT Rat VRRP-1 (VR2) capsaicin receptor.
XX
XX
XX
XX VR1: capsaicin receptor; VR2: VRRP-1; analgesic; diagnosis;
XX human disease; painful syndrome.
XX Rattus rattus.
XX
XX W09909140-A1.
XX
XX 25-FEB-1999.
XX
XX 20-AUG-1998; 98WO-0517466.
XX
XX 22-JAN-1998; 98US-0072151.
XX 20-AUG-1997; 97US-0915461.
XX
XX (REGC ) UNIV CALIFORNIA.
XX
XX Brake A, Caterina M, Julius DJ;
XX
XX WPI; 1999-181023/15.
XX N-PSDB; AAX19730.
XX
XX New capsaicin receptor polypeptide - useful for screening or
XX characterizing capsaicin receptor-binding compounds
XX
XX Claim 4; Page 78-79; 99pp; English.
XX
XX The present sequence is an isolated capsaicin receptor polypeptide
XX (1). Capsaicin polypeptides are useful for identifying binding compounds
XX which affect cellular responses. Preferably this is for identifying a
XX compound that binds (1) and affects a cellular response associated with
XX capsaicin biological activity (e.g. intracellular calcium flux). The
XX polypeptides and host cells are useful for detecting a vanilloid
XX compound (an essential structural component of capsaicin) from natural
XX products by detecting an alteration of intracellular response associated
XX with capsaicin receptor activity, preferably an alteration of
XX intracellular calcium levels, and are useful for screening for compounds
XX for use in analgesics. Capsaicin receptor polypeptides and antibodies
XX are useful for diagnosis and treatment of human diseases and painful
XX syndromes. The transgenic mammals can be used to screen for capsaicin
XX receptor antagonists and agonists. Prior art methods for screening or
XX characterizing new capsaicin receptor-binding compounds relied on assays
XX using sensory neurons in culture or in intact animals. The new
XX polypeptides provide a more sensitive screen.
XX
XX Sequence 761 AA:

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Query Match 68.8%; Score 3011.5; DB 20; Length 761;
 Best Local Similarity 72.0%; Pred. No. 1e-253;
 Matches 598; Conservative 62; Mismatches 93; Indels 77; Gaps 8;

```

QY 1 MTSSSSPVRLFTLDGGDEGSEADRGKIDFGSGLPMPESQFGEDKKFAPQIRVNLY 60
DB 1 mtaasspparlrleldsgdeegnaevnkykge-----ppmespfqredrnspqikvnlntf 56
QY 61 -----RKGTGA-SQDPNPRFDRDLFNVAWSRGVPAGAGATCTGCTGACTCCAGAGTAC 115
DB 57 lkrpkrtsapsqgeprfdtrdrfsvvsrgvp----- 89
QY 116 CTGAGCAAGACGACCAAGTACTCACCAGCTCGEDLAGLPEYLSKTSKYLTDSEYEGST 175
DB 90 -----eeltgllleylrwnskyltdsaytegst 116
QY 176 GKTCIMKAVLNKDGYNACTLPLOIDRDGSGNPQPLVNAOCTDYYRGSALHIAIEKRS 235
DB 117 gktclmkavlnldqgyvacimpilqldkdsnpkplvnaqctdefygshahialekrs 176
QY 236 LQCVKLLVENGANVHARACGRFQKGQCTFYFGEPLPLSLAACKQMDVYSLLENPHOP 295

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Db 177 lgcckllvengadvhlaicgrfifqkngctfysgelpslsaaackgqdvvclyllmnpbq 236
QY 296 ASLOATDSOGNTVLHALVMSIDNSAENIALVTSMDGLAQAGARLCTPTVOLEDIRNODL 355
237 asleatdsalgtvthalyvmsdnasenaialvtsmdglqagarlctptvolesnbgql 236
QY 356 TPLKLAKEGKIEFRHITLQRESG--LSHLSKRFTKTCYGPVRSVSLDASVDSCEENSV 414
297 tplklaekgkiefrihltlqresgpyqpslkrftewcypvrsvslsdsvdsweknsv 356
QY 415 LEIIAFKSPHRRBMVLYLEPLNKLQAKMDLIPKFEMLNLTLYMFTFAVHQPT 474
357 leiafksprhrrbmvllyleplnklqekwdrivsrftfacylymftfvaaynqps 416
QY 475 LKROAPHLKAEVNSMLTGHILLIGIYLLVGLQMLYMRHRVFMISFIDSEIIF 534
417 ldgpalpskatgessmlllghllylllqglwyfwrrllfwisfmdsfellf 476
QY 535 LFOALTVVSQVLCFLAIENYLPPLVSALVGLMLNLTYTRGFQHTGYSVMIOKYLKD 594
477 llqalltlvsgvlrftmetevypllvslvlgwlnllytrfgfghqlysvmlqkylld 536
QY 595 LARPLLYVFLFGFANALVSLQSEAMRPAPFGPNATESVOEGEDGNGAQIRGL 654
537 llflllylvllfifavalslrsrearspkapedninstvteqplvqgee--papyrsll 594
QY 655 EASLEKFTIGGELAFQEOHFRGVNLLLAAYVLTITLLNMLIAMSTVSNVAT 714
595 daalelftkifimgelaifgqrlftrgvallllyavlllylllmllamsetvnhvad 654
QY 715 DSNISIMKQRAISVLEMGNYMC--RRKQAGVMTVGTRKPDGSPDERMCFRVEEYMMAS 773
655 nsvsiwklqraislvemngywwcrrkkhregfllkyvtrtgdtgdpderwcftrveeunwa 714
QY 774 WEOTPLTCLDPSGAGVPRLENPVLASPKKEDEGASENYPVOLLOS 823
715 weotpltdpsgagvprlennpvlaspkkesedgaseenypvollos 715
Db 715 weotpltdpsgagvprlennpvlaspkkesedgaseenypvollos 715

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RESULT 11

AA06560
ID AA06560 standard; Protein; 727 AA.

XX AC AA06560;

XX DT 08-OCT-1999 (first entry)

XX DE Human vanilloid receptor-related polypeptide 1 (VRP-1).

XX KW Vanilloid receptor-related polypeptide 1; VRP-1; VR2;

XX KM capsaicin receptor; VR1; human; vanilloid; analgesic; pain;

XX XX Inflammation; therapy; diagnosis.

OS Homo sapiens.

XX XX Location/Qualifiers

XX FH Key MISC-difference 194..208

XX FT MISC-difference 308 /note= "unidentified residues"

XX FT MISC-difference 311 /note= "unidentified residue"

XX FT MISC-difference 311 /note= "unidentified residue"

XX FT MISC-difference 343..368 /note= "unidentified residues"

XX FT MISC-difference 404 /note= "unidentified residue"

XX FT MISC-difference 460..474 /note= "unidentified residues"

XX FT MISC-difference 558 /note= "unidentified residue"

XX FT MISC-difference 608 /note= "unidentified residue"

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XX XX
PN W0937675-A1.
XX 29-JUL-1999.
PD 22-JAN-1999; 99MO-US01418.
PF 22-JAN-1998; 98US-0072151.
PR (REGC ) UNIV CALIFORNIA.
PA Brake AJ, Caterina M, Julius DJ,
XX WPI; 1999-469113/39.
XX
PT New isolated capsaicin receptor polypeptide and related nucleic acid
PT - useful for detecting vanilloid compounds, identifying modulators,
XX and in diagnosis or treatment of e.g. pain and inflammation
XX
PS Claim 4; Page 91-93; 120pp; English.
XX
CC The present, claimed sequence represents a human vanilloid receptor-
CC related polypeptide 1 (VRP-1 or VR2) sequence predicted from
CC available EST sequences (see AAX97499-501). VRP-1 (see also AA06559)
CC is an example of a capsaicin receptor-related polypeptide of the
CC invention. It is not activated by capsaicin or heat, but may
CC interact with the novel capsaicin receptor VR1 (see AA06558). The
CC invention provides capsaicin receptor and capsaicin receptor-
CC related polypeptides and polynucleotides, as well as expression
CC vectors, host cells and transgenic animals. It also provides a
CC method of using such receptors to identify vanilloid compounds in
CC natural products or to screen candidate compounds that modulate
CC capsaicin receptor function for use as analgesics (vanilloid
CC analogues, therapeutic antibodies, antisense oligonucleotides,
CC capsaicin receptor-encoding polynucleotides for gene therapy),
CC flavour-enhancing agents, etc. Capsaicin receptor-related
CC polypeptides and specific antibodies can also be used for the
CC diagnosis and treatment of human disease and pain.
XX
SO Sequence 727 AA.

```

Query Match 68.5%; Score 2996.5; DB 20; Length 727;
Best Local Similarity 73.5%; Pred. No. 28-252;
Matches 620; Conservative 5; Mismatches 82; Indels 137; Gaps 11;

```

QY 1 MTSPPSSPYFRLETLDDGDEGSEADRGKLDRESGSLPPHESQOGEDRKFPAPIRVNLNY 60
Db 1 mtsppsspyfrletlddggedseadrgrkldfsgslpmpesqfgedrkfapqirvnlly 60
QY 61 RKGTGASQDPNRFDRDLRFNNAVSRGVPGAGATCGGCTGACCTCCAGAGACTGAG 120
Db 61 rkgtgasqdpnrfdrdlrfnnavsrvgpvgagatcggtcgactccagagactgag 120
QY 121 CAAGACGACGAACTACCTCACCAGCTCGEDLAGLPETLSKTSKYLTDSYETEGSTGTC 180
Db 89 -----edaglpelylaktskyltdsyetegstgctcl 120
QY 181 MKAVNLKGVNACILPILQIDRDSGNPOPLVNAOCTDYYRGHSLHLAIEKRSLQCYK 240
Db 121 mkavnlkdvvnacilpqlqdrdsnpplvnaqctddyrgshslhlaiekrslqcyk 180
QY 241 LLEVNGANVHARACGRFFQKGGGTCTCFEELPLSLAACRKMDDVSYLLENPQPSLQA 300
Db 181 lllvnganvharaxxxxxxxxxxxxxxxxxxgelpslaaackqdvvsyllenpqpsslqa 240
QY 301 TDSQGNVTLHALVMSIDNSAENIALVTSMDGLAQAGARLCTPTVOLEDIRNODLPLKL 360
Db 241 tdsqgnvthalyvmsdnasenaialvtsmdglqagarlctptvolesnbgql 300
QY 361 AKKEGKIEIF-RHIL-QREFSGLS-HLSKRFTK-FWYGVVRSVSLVLAVDSCSEENSVLE 416
Db 301 aakegkixlfxrhilaaqfsglkkppfprkftewwlmgprvrvxxxxxxxxxxxxxxxxxx 360

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OY 417 IIAFHCKSPHHRMNVLEPLINKLQAKMDLIRKFLNFCNLIMFTFAVAHQPPLK 476
DB 361 xxxxxxxxpdhrmvmvlepnlkllqakwdlllpkflfnlcnlxymflfavaayhqpplk 420
OY 477 KOAAPHLKAEVNSMLTGHILLGSIYLLVGOLMYFMR-----HVF 520
DB 421 kgaaaplkaevnsmlltghlllllgyllyvgqkwkfwxxxxxxxpfn-- 478
OY 521 IWSIFDSYFEILFLQALLTVVSQVLCFLAEWYLPDLVSALVGLMNLTYTRGFQHT 580
DB 479 -----rvvpapacvca---gaglaepalltytl-----pahrl 509
OY 581 GIYSVMIQKYLIDRLRFLILYLVFLGFAVALVSLSQEAMRPAAPGPNATESVQPMEG 640
DB 510 qchd-----pealvslsqd--wrpeapcpnatatesvqpmeg 543
OY 641 QDEDEGNAQYRGILTEASLELFTTIGMGEIAFOELHFRGVLLLLAYVLLTYILLNM 700
DB 544 qedeqngaqyrgllxaslelftftigmelaifeqhlfrgmvllyllayvlltyllllnm 603
OY 701 LIALMSEYNSVATDSWSIWKLOKAIISVLEMENGYWMCRRKORAGVMLTVGTRPDGSPDE 760
DB 604 lialxsetvnsvaldswwsklqkalsvlemengywwcrkkqragvmltygtkpdgspe 663
OY 761 RMCFRYEVNWSAMEQTLPLCEDPSGAGVPRILENVLASPREDEGASEENYVVO 820
DB 664 rwcfrvevnmawaseqtlplcedpsgagvprtlempvasppkdedgsaenyyvvo 723
OY 821 LOSN 824
DB 724 lqsn 727

RESULT 12
AAM99798
ID AAM99798 standard; Protein; 727 AA.
AC AAM99798;
XX
XX 16-JUN-1999 (first entry)
XX
XX Human VRRP-1 (VR2) capsalcin receptor.
XX
XX VRL: capsalcin receptor; VR2: VRRP-1; analgesic; diagnosis;
XX human disease; painful syndrome.
XX
XX Homo sapiens.
XX
XX MO9909140-A1.
XX
XX 25-FEB-1999.
XX
XX 20-AUG-1998; 98MO-US17466.
XX
XX 22-JAN-1998; 98US-0072151.
XX 20-AUG-1997; 97US-0915461.
XX
XX (REGC ) UNIV CALIFORNIA.
XX
XX Brake A, Caterina M, Julius DJ;
XX
XX WPI: 1999-181023/15.
XX
XX New capsalcin receptor polypeptide - useful for screening or
XX characterizing capsalcin receptor-binding compounds
XX
XX Claim 4; Page 86-88; 99pp; English.
XX
XX The present sequence is an isolated capsalcin receptor polypeptide
XX (1). Capsalcin polypeptides are useful for identifying binding compounds
XX which affect cellular responses. Preferably this is for identifying a
XX compound that binds (1) and affects a cellular response associated with

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CC capsalcin biological activity (e.g. intracellular calcium flux). The
CC polypeptides and host cells are useful for detecting a vanilloid
CC compound (an essential structural component of capsalcin) from natural
CC products by detecting an alteration of intracellular response associated
CC with capsalcin receptor activity, preferably an alteration of
CC intracellular calcium levels, and are useful for screening for compounds
CC for use in analgesics. Capsalcin receptor polypeptides and antibodies
CC are useful for diagnosis and treatment of human diseases and painful
CC syndromes. The transgenic mammals can be used to screen for capsalcin
CC receptor antagonists and agonists. Prior art methods for screening or
CC characterizing new capsalcin receptor-binding compounds relied on assays
CC using sensory neurons in culture or in intact animals. The new
CC polypeptides provide a more sensitive screen.
XX
XX Sequence 727 AA:
SQ

Query Match 68.5%; Score 2996.5; DB 20; Length 727;
Best Local Similarity 73.5%; Pred. No. 2e-252;
Matches 620; Conservative 5; Mismatches 82; Indels 137; Gaps 11;

OY 1 MTSPPSPVRLETLDDGSGDSDRGKLDPSGLPSPMSQFOGDEURKAPQIRVNLNT 60
DB 1 mtsppspvrleclldgsgdsgsdaadgkldfsglpsmsqdfgedrklapqirvnlnt 60
OY 61 RKGTSASPDPRNRRDRRLFNAYSRGVPGAGATCTGCTGACTTCAGAGTACTGAG 120
DB 61 rkgtasapdpnrdrdrlnfnaysrgvpgagatctgctgacttcagagtagtactgag 88
OY 121 CAAGACGACGAGTACTGACCTGCGEDLAGLPEYLSKTSKYLNDSEYTGSTGKTCL 180
DB 89 -----edlaglpeylsktskylndseytgsstgktcl 120
OY 181 MKAIVNLKDGVMACILPLDIDRDSGNPQPLVNAQCDDYRRGSHALHIAEKRSLOCVK 240
DB 121 mkavnlkdgvnmacilplldidrdsgnpqplvnaqcddyrrgshalhialekrslocvk 180
OY 241 LLYENGANVHARACGRFFQKGTCEYFGEPLSLAAGTQMPVSYLLENPQPSLOA 300
DB 181 llyengannvharacgrffqkggtceyfgelplslaagtqmpvstylleppqpsloa 240
OY 301 TDSQGNVTHALVWISDSENIALVTSMTDGLQAGARLCPTVQLEDIRNLDLTPKL 360
DB 241 tdsqgnvthalvwmisdseinalvtsmtdglqagarlcpvqedirnlldltpkl 300
OY 361 AAKEGRIEIR-RHIL-QRESGLS-HLSKRFTE-WCYGPVRSVLYDLASVDSCEANSVLE 416
DB 301 aakegrirleir-rhil-qresgls-hlskrfte-wcygpvrsvlydlasvdsceansvle 360
OY 417 IIAFHCKSPHHRMNVLEPLINKLQAKMDLIRKFLNFCNLIMFTFAVAHQPPLK 476
DB 361 xxxxxxxxpdhrmvmvlepnlkllqakwdlllpkflfnlcnlxymflfavaayhqpplk 420
OY 477 KOAAPHLKAEVNSMLTGHILLGSIYLLVGOLMYFMR-----HVF 520
DB 421 kgaaaplkaevnsmlltghlllllgyllyvgqkwkfwxxxxxxxpfn-- 478
OY 521 IWSIFDSYFEILFLQALLTVVSQVLCFLAEWYLPDLVSALVGLMNLTYTRGFQHT 580
DB 479 -----rvvpapacvca---gaglaepalltytl-----pahrl 509
OY 581 GIYSVMIQKYLIDRLRFLILYLVFLGFAVALVSLSQEAMRPAAPGPNATESVQPMEG 640
DB 510 qchd-----pealvslsqd--wrpeapcpnatatesvqpmeg 543
OY 641 QDEDEGNAQYRGILTEASLELFTTIGMGEIAFOELHFRGVLLLLAYVLLTYILLNM 700
DB 544 qedeqngaqyrgllxaslelftftigmelaifeqhlfrgmvllyllayvlltyllllnm 603
OY 701 LIALMSEYNSVATDSWSIWKLOKAIISVLEMENGYWMCRRKORAGVMLTVGTRPDGSPDE 760
DB 604 lialxsetvnsvaldswwsklqkalsvlemengywwcrkkqragvmltygtkpdgspe 663

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OY 761 RMCFRVEEVMNWSMEQTLPTCEDPSSGAGVPRTEENPLASPKREDEGASEENVYVQOL 820
 DB 664 IWCIFVEEVMNWSMEQTLPTCEDPSSGAGVPRTEENPLASPKREDEGASEENVYVQOL 723
 OY 821 LOSN 824
 DB 724 Iqsn 727
 RESULT 13
 AAY97359
 ID AAY97359 standard; Protein: 436 AA.
 AC AAY97359;
 DT 05-SEP-2000 (first entry)
 DE Human VR-2 (alternate form) partial protein.
 KW VR-2; human; vanilloid receptor; nociceptor; pain signalling;
 KM hyperalgesia; musculoskeletal disorder; neuropathic pain;
 XX chromosome 17p11-12; gene therapy.
 OS Homo sapiens.
 PN MO200029577-A1.
 PD 25-MAY-2000.
 XX 12-NOV-1999; 99MO-US26701.
 PF 13-NOV-1998; 98US-0108322.
 PR 28-DEC-1998; 98US-0114078.
 PR 26-FEB-1999; 99US-0258633.
 PR 19-OCT-1999; 99US-0421134.
 XX (MILL-) MILLENNIUM PHARM INC.
 PA Curtis RAJ;
 PI WPI; 2000-387790/33.
 DR N-PSDB; AAY97359.
 XX New capsaicin/vanilloid receptor polynucleotides and polypeptides, used
 PT to modulate pain signalling mechanisms
 PS Claim 11; Fig 3; 183pp; English.
 XX The present sequence is the partial sequence for an alternate form of
 CC human capsaicin/vanilloid receptor VR-2, which is involved in pain
 CC signalling. The coding sequence was isolated by searching a heart
 CC cDNA library for genes encoding novel receptors of the
 CC capsaicin/vanilloid family, and has been shown to be located at
 CC chromosome 17p11-12. This region has been associated with myasthenia
 CC gravis, Smith-Wagenis syndrome, COBDS, Cone-rod dystrophy, choroidal
 CC dystrophy, central areolar and retinal cone dystrophy, and it is possible
 CC that the protein may be used to treat or diagnose these disorders. In
 CC addition, the gene, protein and its antibodies can be used to diagnose
 CC and treat hyperalgesia, inflammation, infection, ischaemia, joint pain,
 CC tooth pain, headaches, pain associated with surgery or neuropathic pain,
 CC possibly via the use of gene therapy.
 XX Sequence 436 AA;
 Query Match 51.2%; Score 2240; DB 21; Length 436;
 Best local Similarity 76.5%; Pred. No. 8.6e-187;
 Matches 436; Conservative 0; Mismatches 0; Indels 134; Gaps 1;
 OY 255 GRFFQKGQGTCTFFGELPLSLAAGTQWMDVSYLLENPHQAPSLQATDSOGNTVLHALVY 314
 DB 1 griffsgqscfgyfgelplslactkwmdvsvyllenphqpalqatdsqntvlnalvym 60

OY 315 ISDNASAINALVITSMYDGLQAGARLCPVQLEDIRNLQDLPPLKAKECKIEIFRHIL 374
 DB 61 isdnasainalvitsmygllqagarlcpvqledirnlqdltpklkaekgkiefihl 120
 OY 375 QREFSGLSHSRKRTKTCWCGVRSLYDLASVDCSENSVLEITAFHCKSHRRRAVLE 434
 DB 121 qreftsglshsrkrtkwcwgvrvslydlasvdcseensvleitaafhckshrrrmvle 180
 OY 435 PLNKLQAKMDLIPKFFLFLCNLIYMFITTAVAHOPFLKQAAPLKAKEGNSMLLT 494
 DB 181 plnklqakmdltpkfflflcnliymfittavaynpclkaqaaplkaevgnsmllt 240
 OY 495 GHILLILGGITLVGQLMYFRRHVFRTWISFIDSYFEILFLQALTVVSOVLCELAIEW 554
 DB 241 ghillilggitylvqglwyfwrhvfllwstfidsyfelliifqalltvvsgvlcelaw 300
 OY 555 YLPLVSAALVGMNLVYTRGFQHTGITSMTICKVILRLRLLYLVLFQFANAALV 614
 DB 301 ylpvlvsaalvgnnlvyrgrfhtgitsmtickvillrlrllylvlfqfanaalv 335
 OY 615 SLQGEAWRPAPTPGNATESVQPMEGQEDGNGAQYRGILEASLEPKFTIGMGLAEFOE 674
 DB 336 ----- 335
 OY 675 QLHFRGNVLLLLAYVLLTYILLNMLIAMSFTVNSVATDSMSIWKLKALSYLEMENG 734
 DB 336 -----kalsylemg 346
 OY 735 YWMCRRKQRAQVMTVCTKDGSPDERKCRVEEVMNWSMEQTLPTCEDPSSGAGVPRTL 794
 DB 347 ywmcrrkqraqvmtvctkdgsperkcrveevmnwsmeqtlptcedpsgagvprtl 406
 OY 795 ENPLASPKREDEGASEENVYVQLOSN 824
 DB 407 enplaspkredgaseenvypvqlqsn 436
 RESULT 14
 ID AAY97360
 ID AAY97360 standard; Protein: 554 AA.
 AC AAY97360;
 DT 05-SEP-2000 (first entry)
 DE Rat partial VR-2 protein.
 KW VR-2; rat; vanilloid receptor; nociceptor; pain signalling;
 KM hyperalgesia; musculoskeletal disorder; neuropathic pain;
 XX gene therapy.
 OS Rattus sp.
 PN MO200029577-A1.
 PD 25-MAY-2000.
 XX 12-NOV-1999; 99MO-US26701.
 PF 13-NOV-1998; 98US-0108322.
 PR 28-DEC-1998; 98US-0114078.
 PR 26-FEB-1999; 99US-0258633.
 PR 19-OCT-1999; 99US-0421134.
 XX (MILL-) MILLENNIUM PHARM INC.
 PA Curtis RAJ;
 PI WPI; 2000-387790/33.
 DR N-PSDB; AAA30256.
 XX New capsaicin/vanilloid receptor polynucleotides and polypeptides, used
 PT to modulate pain signalling mechanisms

XX Claim 11; Fig 4; 183pp; English.

PS The present sequence is the protein sequence for the rat
 CC Capsaicin/vanilloid receptor VR-2, which is involved in pain signalling.
 CC The coding sequence was isolated by searching a dorsal root ganglion
 CC library for genes encoding novel receptors of the capsaicin/vanilloid
 CC family. The human version of this gene is found at chromosome 17p11-12, a
 CC region which has been associated with myasthenia gravis, Smith-Magenis
 CC syndrome, CORDS, Cone-rod dystrophy, choroidal dystrophy, central areolar
 CC and retinal cone dystrophy, and it is possible that the human protein may
 CC be used to treat or diagnose these disorders. In addition, the human
 CC gene, protein and its antibodies can be used to diagnose and treat
 CC hyperalgesia, inflammation, infection, ischaemia, joint pain, tooth pain,
 CC headaches, pain associated with surgery or neuropathic pain, possibly via
 CC the use of gene therapy.

XX Sequence 554 AA:

Query Match 51.0%; Score 2230; DB 21; Length 554;

Best Local Similarity 79.0%; Pred. No. 9e-186; Mismatches 66; Indels 8; Gaps 4;

Matches 437; Conservative 42; Mismatches 66; Indels 8; Gaps 4;

273 LSLACTKQMDVSVLLENPHQPSAQATDSQGNVYLHALVMSDMSAENIALVTSMYTG 332
 7 LSLACTKQMDVSVLLENPHQPSAQATDSQGNVYLHALVMSDMSAENIALVTSMYTG 332

333 LLAGARLCPYVQLDELRLQDLPLKLAKEGKIEIFRHILQREFSG-LSHLRKFTEM 391
 67 LLAGARLCPYVQLDELRLQDLPLKLAKEGKIEIFRHILQREFSG-LSHLRKFTEM 391

392 CYGPVRSVLYLSDVSCENSVLELIAFHCKSPHRRMVLEPLNKLQAKWDLIPKE 451
 127 CYGPVRSVLYLSDVSCENSVLELIAFHCKSPHRRMVLEPLNKLQAKWDLIPKE 451

452 PLNFCLNLIYMFPAVAVHOPTLKKQAPHLKAEVNSMLTGHILLGGIYLLVGL 511
 167 PLNFCLNLIYMFPAVAVHOPTLKKQAPHLKAEVNSMLTGHILLGGIYLLVGL 511

512 WYFMRHVFIMVIFSDYFEILFQALITVVSQVLCFLAEMVYPLVASVLTGLNLL 571
 247 WYFMRHVFIMVIFSDYFEILFQALITVVSQVLCFLAEMVYPLVASVLTGLNLL 571

572 YTRGFOHTGTVSVMIQVYILRDLRFLLIYVLFGEFAVALVLSQEAARPEAPTPMA 631
 307 YTRGFOHTGTVSVMIQVYILRDLRFLLIYVLFGEFAVALVLSQEAARPEAPTPMA 631

632 TESVOPMEGDEGNGAOYRGILEASLELFEKFTTGMELAFQEOQLHFRGMVLLLLAVL 691
 367 TESVOPMEGDEGNGAOYRGILEASLELFEKFTTGMELAFQEOQLHFRGMVLLLLAVL 691

692 LTYILLMLLALINSEETNSVATDSMSIMKLOKATSVLEMENGYWMC-RKKRAGVMTLV 750
 425 LTYILLMLLALINSEETNSVATDSMSIMKLOKATSVLEMENGYWMC-RKKRAGVMTLV 750

751 GTRPDSPDERMCFEVEENNASMEQTLPTLCEPDSGAGVPTLENPVLASPKDEDDA 810
 485 GTRPDSPDERMCFEVEENNASMEQTLPTLCEPDSGAGVPTLENPVLASPKDEDDA 810

811 SEENVVPVQLLOS 823
 541 SEENVVPVQLLOS 823

RESULT 15
 AAY06561 standard; Protein; 843 AA.
 AAY06561;
 08-OCT-1999 (first entry)

DE Chicken capsaicin receptor subtype VR1.

XX Capsaicin receptor; VR1; vanilloid-like receptor 1; analgesic;

KW pain; inflammation; therapy; diagnosis; chicken.

XX Gallus sp.

XX MO9937675-A1.

XX 29-JUL-1999.

XX 22-JAN-1999; 99MO-US01418.

XX 22-JAN-1998; 98US-0072151.

XX (REGC) UNITV CALIFORNIA.

XX Brake AJ, Caterina M, Julius DJ;

XX WPI; 1999-469113/39.

XX N-PSDB; AAX87503.

PT New isolated capsaicin receptor polypeptide and related nucleic acid
 PT - useful for detecting vanilloid compounds, identifying modulators,
 PT and in diagnosis or treatment of e.g. pain and inflammation
 PS Claim 4; Page 97-99; 120pp; English.

CC The present sequence represents chicken capsaicin receptor subtype
 CC VR1 (vanilloid-like receptor 1). The invention provides capsaicin
 CC receptor and capsaicin receptor-related polypeptides and
 CC polynucleotides, as well as expression vectors, host cells and
 CC transgenic animals. It also provides a method of using such
 CC polypeptides to identify vanilloid compounds in natural products or
 CC to screen candidate compounds that modulate capsaicin receptor
 CC function for use as analgesics (vanilloid analogues, therapeutic
 CC antibodies, antisense oligonucleotides, capsaicin receptor-encoding
 CC polynucleotides for gene therapy), flavour-enhancing agents, etc.
 CC Capsaicin receptor polypeptides and specific antibodies can also be
 CC used for the diagnosis and treatment of human disease and pain.

XX Sequence 843 AA:

Query Match 37.7%; Score 1649; DB 20; Length 843;

Best Local Similarity 43.8%; Pred. No. 7.3e-135; Mismatches 218; Indels 124; Gaps 13;

Matches 358; Conservative 118; Mismatches 218; Indels 124; Gaps 13;

4 PSSPVFRLETLIDGQEDGSEADRGKLT--DFGSGLPWESQFQGEDRRFAPQ-IRVNLN 59
 49 pksnlf-----arrgrfmgdcckmepndsfyq-mdhlmavsvtkfhan 93

60 YKKG-----TGASQDPNPRDRDLFNNAVSRGVGAGATCTGGCTGACTTCC 108
 94 meryglhklilstdsitgcekafkfydrirrfidavary----- 131

109 AAGAGACCTGACGACAGACGACGACTCTACCGACTGEGDLAPLEYLSTSKYINDS 168
 132 -----stkdlddlilylnrltlhltdd 153

169 EYTESGTGCTCMAKAVNLKDGVNACILPLQIDRDSGNPQPLVNAACDDYYRGSHALH 228
 154 efkepetgkctcllkamlnhbgkndtllpdlldakktgtlcfvnaeyrdnykqgtalh 213

229 IAIKRSLOCVKLVENGANVHARACGRFQKGG-TCFYEGELPLSLAACKTQMDVSVY 287
 214 IAIKRSLOCVKLVENGANVHARACGRFQKGG-TCFYEGELPLSLAACKTQMDVSVY 287

288 ILENPHOPASLQATDSQGNVYLHALVMSDMSAENIALVTSMYDGLDAGARLCTVQLE 347
 274 ILENPHOPASLQATDSQGNVYLHALVMSDMSAENIALVTSMYDGLDAGARLCTVQLE 347

348 DIRNLDLPLKLAKEGKIEIFRHILQREFSG--LSHLRKFTEMCGPVRSVLYDLAS 405

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Db 334 .eltnkqgltpcltlaakgkigtifayllrrreikdeecrhlsrkftewaygpyhslydlsc 393
QY 406 VDSCEENSVEIITIAFHCKSPHRHRVLEPLNKLLQAKWDLIPK-FELNFCNLIMFT 464
Db 394 ldtceksvlellayssetpnrhemllveplnllgdkwdrfvkhlfyfnffviahls 453
QY 465 FTAVAYQPTLKKQAPH-LKAEVGNMMLTGHLILGSIYLLVGOLMFWRHAFIWI 523
Db 454 ltaayyrrpqkqdkpfafighstgeyfrvtgelisvlg9lyffirg1qyfvqirpslkt 513
QY 524 SFIDYFEILFLFOALLTVVSQVLCFLAIEWYPLIYSALVGLWNLVYTRGFOHGIY 583
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QY 584 SVMIOKYLRLFLILYVFLFGFAVALVSLSQEAMRPEAPTPGNATESVQPMGQED 643
Db 574 svmlakmlrlclcrfmfyivfljgfstavtllcd-----dnegqdc 616
QY 644 EGN-----GAQYRGILEASLELEFKFTIGMGEIARFQEOUHRGWLILLAVLL 692
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QY 693 TYILLNMLTALMSEFYNSVATDSWSIMKLOKAIISVLEMENGYWMC-RKQORAGVMLTVG 751
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Search completed: October 3, 2001, 17:33:45
 Job time: 158 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: October 3, 2001, 17:31:37 ; Search time 13.87 Seconds
(without alignments)
1223.248 Million cell updates/sec

Title: US-09-445-614-2

Perfect score: 4376
Sequence: 1 MTSPSSSSVFRLFTLDGQE.....EDEDGASEBNVYVQLQSN 824

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 197339 seqs, 20590346 residues

Total number of hits satisfying chosen parameters: 197339

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents,AA:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	1622.5	37.1	839	4	US-09-197-636-2
2	1621.5	37.1	839	4	US-09-197-636-8
3	1615.5	36.9	839	4	US-09-197-636-4
4	202	4.6	143	4	US-08-990-823-112
5	200.5	4.6	1345	2	US-08-977-767-3
6	183.5	4.2	801	1	US-07-906-349A-6
7	180	4.1	120	3	US-08-508-761B-22
8	169	3.9	341	2	US-08-209-521-11
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11	151	3.5	1839	2	US-09-172-977-4
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16	138.5	3.2	352	3	US-09-065-474-139
17	138.5	3.2	1745	2	US-08-031-485-33
18	138.5	3.2	1745	2	US-08-847-429A-33
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22	137	3.1	1533	3	US-08-933-774-9
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24	134.5	3.1	58	1	US-08-279-058B-23
25	133	3.0	45	1	US-08-451-947-97
26	133	3.0	45	2	US-08-424-826A-97
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28	133	3.0	45	5	PCT-US91-06950-97	Sequence 97, Appl
29	131	3.0	303	2	US-09-031-485-23	Sequence 23, Appl
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33	129	2.9	47	3	US-08-482-085B-91	Sequence 91, Appl
34	127.5	2.9	55	3	US-08-476-509B-46	Sequence 46, Appl
35	127	2.9	51	3	US-08-482-085B-90	Sequence 90, Appl
36	127	2.9	75	3	US-08-482-085B-72	Sequence 72, Appl
37	127	2.9	300	4	US-08-897-340-32	Sequence 32, Appl
38	127	2.9	300	4	US-09-252-329-32	Sequence 32, Appl
39	126	2.9	348	2	US-09-031-485-28	Sequence 28, Appl
40	126	2.9	348	2	US-08-847-429A-28	Sequence 28, Appl
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42	126	2.9	394	2	US-08-555-568B-17	Sequence 17, Appl
43	126	2.9	551	3	US-08-699-103B-25	Sequence 25, Appl
44	126	2.9	687	2	US-08-555-568B-21	Sequence 21, Appl
45	126	2.9	3075	2	US-08-460-309-5	Sequence 5, Appl

ALIGNMENTS

RESULT 1
US-09-197-636-2
; Sequence 2, Application US/09197636
; Patent No. 6239267
GENERAL INFORMATION:
APPLICANT: DUCKWORTH, DAVID
APPLICANT: HAYES, PHILIP
APPLICANT: MEADOWS, HELEN
APPLICANT: DAVIS, JOHN
TITLE OF INVENTION: NOVEL COMPOUNDS
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ratner & Prestia
STREET: P.O. Box 980
CITY: Valley Forge
STATE: PA
COUNTRY: US
ZIP: 19482-0980
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/197,636
FILING DATE: 23-NOV-1998
CLASSIFICATION:
Prior Application DATA:
APPLICATION NUMBER: UK 9805137.8
FILING DATE: 12-MAR-1998
APPLICATION NUMBER: UK 9815791.0
FILING DATE: 21-JUL-1998
APPLICATION NUMBER: UK 9819278.4
FILING DATE: 03-SEP-1998
ATTORNEY/AGENT INFORMATION:
NAME: Prestia, Paul F
REGISTRATION NUMBER: 23,031
REFERENCE/DOCKET NUMBER: GP-30075
TELECOMMUNICATION INFORMATION:
TELEPHONE: 601-407-0700
TELEFAX: 610-407-0701
TELEX: 846169
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 839 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-197-636-2

Query Match	37.1%;	Score 1622.5;	DB 4;	Length 839;
Best Local Similarity	40.8%;	Pred. No. 2.3e-128;		
Matches 339;	Conservative 117;	Mismatches 194;	Indels 45;	Gaps 11

[illegible]

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1 COMPUTER READABLE FORM:
2 MEDIUM TYPE: IBM Diskette
3 COMPUTER: IBM Compatible
4 OPERATING SYSTEM: DOS
5 SOFTWARE: FASTSEQ for Windows Version 2.0
6 CURRENT APPLICATION NUMBER: US/09/197,636
7 FILING DATE: 23-NOV-1998
8 CLASSIFICATION:
9 PRIOR APPLICATION DATA:
10 APPLICATION NUMBER: UK 9805137.8
11 FILING DATE: 12-MAR-1998
12 APPLICATION NUMBER: UK 9815791.0
13 FILING DATE: 21-JUL-1998
14 APPLICATION NUMBER: UK 9819278.4
15 FILING DATE: 03-SEP-1998
16 ATTORNEY/AGENT INFORMATION:
17 NAME: Prestia, Paul F
18 REGISTRATION NUMBER: 23,031
19 REFERENCE/DOCKET NUMBER: GP-30075
20 TELECOMMUNICATION INFORMATION:
21 TELEPHONE: 601-407-0700
22 TELEFAX: 610-407-0701
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Query Match	37.1%	Score 1621.5	DB 4	Length 839
Best Local Similarity	48.8%	Pred. No. 2.0e-128		
Matches 339	Conservative 117	Mismatches 194	Indels 45	Gaps 11

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QY	670	LAFQEQHLFRQNVLLLLAYLYLLTYLLLNLLMASETVNSVATSDNSITWKLQKASVL	729
Db	648	LEFENEDFKAVFILLLAYLYLYLLLNLLMASETVNSVATSDNSITWKLQKASVL	707
QY	730	EMENGYMWC-RKKORAGVMLTVGTRPDGSPDERWCERVEEYNNASWQOTLPTECEDSGA	788
Db	708	DTERSPFLCKMKKAPRSGKLLQVGYTPDGKXDYRWCERFVDEYNNATNTNNGIINEDGNC	767
QY	789	-GVPRTLENPLVLPKPEDEDEGASEENYVYQOLQ	822
Db	768	EGVKRTLSFSLRSS-----RVSGRHKMKNFALVPLLR	798
RESULT	2		
	US-09-197-636-8		
	Sequence 8 / Application US/09197636		
	Patent No 6239267		
	GENERAL INFORMATION:		
	APPLICANT: DUCKWORTH, DAVID		
	APPLICANT: HAYES, PHILIP		
	APPLICANT: MEADOWS, HELEN		
	APPLICANT: DAVIS, JOHN		
	TITLE OF INVENTION: NOVEL COMPOUNDS		
	NUMBER OF SEQUENCES: 8		
	CORRESPONDENCE ADDRESS:		
	ADDRESSEE: Ratner & Prestela		
	STREET: P.O. Box 980		
	CITY: Valley Forge		
	STATE: PA		
	COUNTRY: US		
	ZIP: 19482-0980		
QY	149	EDLAGPEYLSKTSKYLTSEYREGSGKCLMKKAVYNLKDGVNACLPLOLIDROSGNP	208
Db	128	ODLESLLFLQSKKHHTDNEFODPETGKTCLLKNMNNLHDGONTTYPILLETARQDSTL	187
QY	209	QPLVNAOCTDDYYRGSHALHAIAREKSLQCVKLLVENGAVNHARACGRFQSGG--TCFY	267
Db	188	KELVNASYFDSYKGGOTALHAIATERNNMALVTLTVENGADVQAAAGDFPKTKGRPGFY	247
QY	268	FGLSLPLSLACTQONOVSYLLENPNQOPASLOATDSOGNTVLAALYISDNSKENTALYT	327
Db	248	FGLSLPLSLACTQOLQIVLFFLLONSWOTADISARDVGNVTALVLALEVADNTADNKRKYT	307
QY	328	SNYDGLLOAGARLCPTVOLEDIRNLQDLPPLKLAAREKGIETFRHILLOREFS--GLSHLS	385
Db	308	SNYNEILLIGAKLHPTLKEELTNKKGMPLALAACTGKGVLYALLOREIOPECRHLS	367
QY	386	RKTEWCYGPVRYSLYDLASVDSCEANSVLEITAF-HCKSPAHNRNVLEPLKLLQAKW	444
Db	368	RKTEMAVGPVHSLDYDLSCIDPCENSNVLEVAYSSETPNHDMLVEPLRLLQDDKW	427
QY	445	DLILPK-FELNPLCNLIYVEIFETAVVYHOPTLKQOAPHLKAE-VGNSMLTLGHILILG	502
Db	428	DREVKRIEYFENFLVYCLYMIIFETAVVYRPV--DGLPPEKMEKTDYFRVYGEILSVIG	484
QY	503	GIYLLVQGLMYFRRHRYFIMISIDSEYFILLFQALLLVVSOVLCFLAIEWLPLLVSA	562
Db	485	GVYFEFRGIQYFLQRRPSKLTVDYSSELPFLOSLFMATVLYVLSHKREVASVMS	544
QY	563	LVGLWNLLYYTRGFQHTGISYVMLOKVLIRDLIRLILLYLVELEFGAVALYSLSQEA--	620
Db	545	LALGWTNMLYTRGFQOMGIYAVMIKMLIRDLCRMFMVYVFLFEGFAVYVTLIEDGNK	604
QY	621	-----WRBPAPGNATSEYQPMGQDEBNGAOYRGILLESLEKFTTGMGE	669
Db	605	DLSPESTSHRMGRPACRPDSS-----YNSLYSTCLELKFRTTGMGD	647

QY 670 LAFQOLHFRGAVLLLLAVLLTYILLNMLALMSETVNSVATDSWSIMKLOKASIVL 729
 Db 648 LEFTEYNDFAVPIILLAVLLTYILLNMLALMSETVNSVATDSWSIMKLOKASIVL 707
 QY 730 EMNGYWMW-RKQORAGVMTLVGTPDGPDERMCFVEEYVNASWQTLPTLCEDPSGA 788
 Db 708 DTEKSLKCMKRAKFRSGKLVQVGTDPGKDDYRWCFFRVDENVTMTNTNVIINDEPGNC 767
 QY 789 -GVPRILENPLASPPKEDGASEENYVPVOLLO 822
 Db 768 EGVKRTLSFSLRSS----RVSGRHMKNFALVPLLR 798

RESULT 3
 US-09-197-636-4
 Sequence 4, Application US/09197636
 Patent No. 6239267
 GENERAL INFORMATION:
 APPLICANT: DICKWORTH, DAVID
 APPLICANT: HAYES, PHILIP
 APPLICANT: MEADOWS, HELEN
 APPLICANT: DAVIS, JOHN
 TITLE OF INVENTION: NOVEL COMPOUNDS
 NUMBER OF SEQUENCES: 8
 CORRESPONDENCE ADDRESSES:
 ADDRESSEE: Ratner & Prestia
 STREET: P.O. Box 980
 CITY: Valley Forge
 STATE: PA
 COUNTRY: US
 ZIP: 19482-0980
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 OPERATING SYSTEM: DOS
 SOFTWARE: FASTSEQ for Windows Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/197, 636
 FILING DATE: 23-NOV-1998
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: UK 9805137.8
 FILING DATE: 12-MAR-1998
 APPLICATION NUMBER: UK 9815791.0
 FILING DATE: 21-JUL-1998
 APPLICATION NUMBER: UK 9819278.4
 FILING DATE: 03-SEP-1998
 ATTORNEY/AGENT INFORMATION:
 NAME: Prestia, Paul F
 REGISTRATION NUMBER: 23,031
 REFERENCE/DOCKET NUMBER: GP-30075
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 601-407-0700
 TELEFAX: 610-407-0701
 TELEX: 846169
 INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 839 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-09-197-636-4

Query Match 36.9%; Score 1615.5; DB 4; Length 839;
 Best Local Similarity 48.6%; Pred. No. 9e-128;
 Matches 338; Conservative 117; Mismatches 195; Indels 45; Gaps 11;

QY 149 EDLAGPEYLSKSKLTSEYEGSTGKCLAKAVLNKQVNAACLPILLOIDRDSGNP 208
 Db 128 QDLSEILFLQKSKKHXTDNFDPETGKTCCLKAMLNLDGNTTIPLLLEIARQDSTL 187

QY 209 QPLVNAOCTDDYYRGSHALHAIERSLQCYKLLVNGANVHARACGRFOGOG--TCFY 267
 Db 188 KELVNAAYTDXYTGQALHAIERRMALVTLVNGADVQAANAHDFKTKGRGCFY 247
 QY 268 FGEPLSLAATQKQMDVSYLLENPHQASLOARDSGNTVHALVMSNSAENIALVT 327
 Db 248 FGEPLSLAATQNLGIVKFLQNSWQTADISARDVGNVYHALVADNTADNTFVY 307
 QY 328 SMYGLLQAARLCPTQVQEDIRNLQDLPKLAAGKKEIFRHHIQREPS--GLSHLS 385
 Db 308 SMYNEILLAKKHPKLELTNRKGMPTPLAAGGKIVLAYILQREIOPEECHLS 367
 QY 386 RKTEWCYGPVRSYLDVADSVSCSENSYLEIAF--CKSPHRRHVVPLNKLQAKN 444
 Db 368 RKTEWAXYGPVHSLYLDSCIDTCEKNSVLEVIAYSSSETPNRHMDLVEPLNLDKN 427
 QY 445 DLILPK-FPLNPLCNLYMEFTAVAAVHOPPLKQAAPHKAE--VGN5MLTGHIILG 502
 Db 428 DREVKRIFFENFLVYCYMIIFTMAAYRPV--DGLPFRMEKTDGYFRVYTGELISVLG 484
 QY 503 GIYLVGQWYFMRHVFVINSFDSFELLFQALLTVYSOYLCPLATEWYIPLVSA 562
 Db 485 GYVFFERGIQYFLQRRSMKTLFVDSYSEMLFLOSLEMLATVLYSHLKEYVASWFS 544
 QY 563 LVLGMLNLVYTRGFQHTGIVSVMIQKILRDLRFLIYVLFQFAVALVLSIOBA-- 620
 Db 545 LALGWTMLLYTRGFQOMGIYAVIEMILRDLRFVYVIFLGSTAVVTLIEGKN 604
 QY 621 -----WRPEAPTGNAESYOPMEGOEDGNGAQRGLIEASLEFFTTIGME 669
 Db 605 DSLPESSTSHRMGPACRPDSS-----YNSLYSCLELFTKTIMGD 647
 QY 670 LAFQOLHFRGAVLLLLAVLLTYILLNMLALMSETVNSVATDSWSIMKLOKASIVL 729
 Db 648 LEFTEYNDFAVPIILLAVLLTYILLNMLALMSETVNSVATDSWSIMKLOKASIVL 707
 QY 730 EMNGYWMW-RKQORAGVMTLVGTPDGPDERMCFVEEYVNASWQTLPTLCEDPSGA 788
 Db 708 DTEKSLKCMKRAKFRSGKLVQVGTDPGKDDYRWCFFRVDENVTMTNTNVIINDEPGNC 767
 QY 789 -GVPRILENPLASPPKEDGASEENYVPVOLLO 822
 Db 768 EGVKRTLSFSLRSS----RVSGRHMKNFALVPLLR 798

RESULT 4
 US-08-990-823-112
 Sequence 112, Application US/08990823D
 Patent No. 6228371
 GENERAL INFORMATION:
 APPLICANT: Nano, Francis
 TITLE OF INVENTION: Mycobacterium tuberculosis DNA Sequences Encoding
 FILE REFERENCE: 49086
 CURRENT APPLICATION NUMBER: US/08/990,823D
 EARLIER FILING DATE: 1997-12-15
 EARLIER APPLICATION NUMBER: US 96/10375
 EARLIER FILING DATE: 1996-06-14
 EARLIER APPLICATION NUMBER: 60/000,254
 EARLIER FILING DATE: 1995-06-15
 NUMBER OF SEQ ID NOS: 113
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO: 112
 LENGTH: 143
 TYPE: PRT
 ORGANISM: Mycobacterium tuberculosis
 US-08-990-823-112

Query Match 4.6%; Score 202; DB 4; Length 143;
 Best Local Similarity 54.3%; Pred. No. 1.2e-09;
 Matches 38; Conservative 0; Mismatches 22; Indels 10; Gaps 4;

OY 89 GAGATCTGCTGGA---CTTCCAGATAC---CTGAGCAAGAC-CAGCAGTACTCTAC 141
 DB 25 GTGACTCAGGACGAGGCCCGCCACGTTGCGGAGCGCGCAATCTTCCCTGTGCTCAC 84
 OY 142 CGACT---CG 148
 DB 85 CGACTTCCG 94

RESULT 5

US-08-977-767-3
 ; Sequence 3, Application US/08977767
 ; Patent No. 5972684
 ; GENERAL INFORMATION:
 ; APPLICANT: Bandman, Olga
 ; APPLICANT: Yue, Henry
 ; APPLICANT: Greenwald, Sara
 ; APPLICANT: Corley, Neil C.
 ; TITLE OF INVENTION: CARBONIC ANHYDRASE VIII
 ; NUMBER OF SEQUENCES: 3
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Incyte Pharmaceuticals, Inc.
 ; STREET: 3174 Porter Drive
 ; CITY: Palo Alto
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 94304
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: DOS
 ; SOFTWARE: FASTSEQ for Windows Version 2.0
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/977,767
 ; FILING DATE: Herewith
 ; CLASSIFICATION: 424
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER:
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Billings, Lucy J.
 ; REGISTRATION NUMBER: 36,749
 ; REFERENCE/DOCKET NUMBER: PF-0423 US
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 650-855-0555
 ; TELEFAX: 650-845-4166
 ; TELEX:
 ; INFORMATION FOR SEQ ID NO: 3:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 1345 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; IMMEDIATE SOURCE:
 ; LIBRARY: GenBank
 ; CLONE: 1532042
 ; US-08-977-767-3

Query Match 4.6%; Score 200.5; DB 2; Length 1345;
 Best Local Similarity 40.7%; Pred. No. 3.8e-08;
 Matches 44; Conservative 0; Mismatches 13; Indels 49; Gaps 6;
 OY 89 GAGGATC---TGGCTGAGCTCC-----AGAGTAC-----C 116
 DB 124 GAGGACCGGAGAGCTGGAAGTCTCGGAGAGGATTTGCAACAAGAGGGGAGAC 183
 OY 117 TGAGC-AAGACCGAGAGTAC-----CTACCGA---CTC 147
 DB 184 TAGAGAGGGCGCGCGGACATTGGAGAGGGGTACCCCGAGGCTC 231

RESULT 6

US-07-906-349A-6
 ; Sequence 6, Application US/07906349A
 ; Patent No. 5434064
 ; GENERAL INFORMATION:
 ; APPLICANT: Schlessinger, Joseph
 ; APPLICANT: Skolnik, Edward Y.
 ; APPLICANT: Margolis, Benjamin L.
 ; TITLE OF INVENTION: A NOVEL EXPRESSION-CLONING METHOD FOR
 ; TITLE OF INVENTION: IDENTIFYING TARGET PROTEINS FOR EUKARYOTIC TYROSINE KINASE
 ; NUMBER OF SEQUENCES: 16
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Biowdy and Nelmark
 ; STREET: 419 Seventh Street, N.W.
 ; CITY: Washington
 ; STATE: D.C.
 ; COUNTRY: USA
 ; ZIP: 20004
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/07/906,349A
 ; FILING DATE: 30-JUN-1992
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 07/643,237
 ; FILING DATE: 18-JAN-1991
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 202-628-5197
 ; TELEFAX: 202-737-3528
 ; INFORMATION FOR SEQ ID NO: 6:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 801 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-07-906-349A-6

Query Match 4.2%; Score 183.5; DB 1; Length 801;
 Best Local Similarity 51.4%; Pred. No. 5e-07; 18; Indels 17; Gaps 5;
 Matches 37; Conservative 0; Mismatches 18; Indels 17; Gaps 5;
 OY 86 GVPGAGATCTGCTGAGCTTCCAG-AGTAC-CTGAGCAAG---ACCAGC---AAGTA 135
 DB 390 GAGGGGCGACCGC-----CCAGTGGGACATGGGAGGTAAACCAACCTTGAAATC 442
 OY 136 CCTACCGACTC 147
 DB 443 CCCACCTCC 454

RESULT 7

US-08-508-761B-22
 ; Sequence 22, Application US/08508761B
 ; Patent No. 6027920
 ; GENERAL INFORMATION:
 ; APPLICANT: Joliff, Gwennael
 ; APPLICANT: Guyonvarch, Arnel
 ; APPLICANT: Purification, Relano
 ; APPLICANT: Duchilton, Francis
 ; APPLICANT: Renaud, Michel
 ; TITLE OF INVENTION: System for Protein Expression and
 ; TITLE OF INVENTION: Secretion Especially in Corynebacteria
 ; NUMBER OF SEQUENCES: 37
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Jacobson, Price, Holman & Stern, PLLC
 ; STREET: 400 Seventh St. N.W.

```

CITY: Washington D.C.
COUNTRY: U.S.A.
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/508,761B
FILING DATE: 31-JUL-1995
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: FR 91/09652
FILING DATE: 29-JUL-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 91/09870
FILING DATE: 02-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: Player, William E.
REGISTRATION NUMBER: 31,409
REFERENCE/DOCKET NUMBER: P58525NA
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 638-6666
TELEFAX: (202) 393-5350
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 120 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: synthetic
US-08-508-761B-22

Query Match
Best Local Similarity 4.18; Score 180; DB 3; Length 120;
Pred. No. 6,5e-08;
Matches 37; Conservative 0; Mismatches 21; Indels 12; Gaps 5;

QY 89 GAGAGTGTGCTGACT---CCAGACTACTGAGCAG-ACC--AGCAGTACTCT--- 138
DB 20 GACCTGTGTGCTGCTGCTGCGCTGCG--CCTGCGCTGTGCTGAGCCTGGGCTGGGC 77
QY 139 CACCGACTCG 148
DB 78 CTGCGCCTGG 87

RESULT 8
US-08-209-521-11
Sequence 11, Application US/08209521
Patent No. 5922855
GENERAL INFORMATION:
APPLICANT: Liskay, Robert M.
APPLICANT: Bronner, C. Eric
APPLICANT: Baker, Sean M.
APPLICANT: Bollag, Ront J.
APPLICANT: Kolodner, Richard D.
TITLE OF INVENTION: MAMMALIAN DNA MISMATCH REPAIR GENES
TITLE OF INVENTION: hMLH1 AND hPMS1
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kolisch, Hartwell, Dickinson, McCormack &
ADDRESSEE: Heuser
STREET: 520 S.W. Yamhill, Suite 200
CITY: Portland
STATE: Oregon
COUNTRY: US
ZIP: 97204
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/209,521
FILING DATE: 08-MAR-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Van Rysselberghe, Pierre C.
REGISTRATION NUMBER: 33,557
REFERENCE/DOCKET NUMBER: OHSU 306A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (503) 224-6655
TELEFAX: (503) 295-6679
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 341 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
POSITION IN GENOME:
MAP POSITION: 3p21.3-23
US-08-209-521-11

Query Match
Best Local Similarity 3.98; Score 169; DB 2; Length 341;
Pred. No. 2,4e-06;
Matches 44; Conservative 0; Mismatches 19; Indels 38; Gaps 8;

QY 82 AVSRGVPAGAGTGTGCT-----GG---ACTTCAGAGTACCTGAGCAGA 125
DB 60 AACAAAGAGATCTGATATGTATGTAAGAGKTCACCTACTAGTAAC---TGC-AGT 115
QY 126 CC-----AGCAGTACTC-ACC---GAC---TCG 148
DB 116 CCTTGAGAGDTTATGACGAGATTCTACCTATGCTTTCG 156

RESULT 9
US-07-609-716-56
Sequence 56, Application US/07609716
Patent No. 5514581
GENERAL INFORMATION:
APPLICANT: Ferraro, Franco A.
APPLICANT: Cappello, Joseph
TITLE OF INVENTION: Functional Recombinantly Prepared
TITLE OF INVENTION: Synthetic Protein Polymer
NUMBER OF SEQUENCES: 118
CORRESPONDENCE ADDRESS:
ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert
STREET: Four Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: CA
COUNTRY: US
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/609,716
FILING DATE: 06-NOV-1990
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Rowland, Bertram I
REGISTRATION NUMBER: 20015
REFERENCE/DOCKET NUMBER: A-55186-3/BIR
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-781-1989
TELEFAX: 415-398-3249
INFORMATION FOR SEQ ID NO: 56:
SEQUENCE CHARACTERISTICS:
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Query Match	3.48;	Score 150;	DB 4;	Length 1088;
Best Local Similarity	32.38;	Pred. No. 0.00051;		
Matches 51; Conservative	24;	Mismatches 51;	Indels 32;	Gaps 6

[illegible]

Query Match	3.4%	Score 148	DB 2	Length 843
Best Local Similarity	27.3%	Pred. NO	0.00053	
Matches 88	Conservative 45	Mismatches 97	Indels 92	Gaps 19

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QY 199 LQIDRDGNGPOPLVNAQCTDDYRGSHALPITALREKSLQCVCTLLVENGAVHNRACGRF 258
Db 348 LLLDK -RANP-----NARALN-----GFFPLHACKKNKIKMELLYKGAIOA----- 391
QY 259 QKGOGCTFYTGELPLSLAAGCTKQMDVSYLLENPHOPASLOATDSOGNTVLAALVMSDN 318
Db 392 -----ITSGSLPPIPAALMGHLNITLLLOH-----GASPDVNNIRETLLHMAA----- 437
QY 319 SAENIALVTSMYGILLQAGARCLPTVLEDIRNLODTPKLAKREKIIIFPHILOREF 378
Db 438 RAGEVEVYRC-----LIRNGA-----LYDARAREETPLHISRCLKTPIYVOLLGH----- 484
QY 379 SGLSHLSRKTECMYCGVYRVSLL-----YDLASVSCSENSVLEIIFAPHCKSPHRHRMAYLE 434
Db 485 --VAHPDPAATNG-YPPPLHISAREGOVDASV-----LLEGAHSHSLATKRG---FT 530
QY 435 PLNKLOAKKDLL-IPKFFL-----NELCNLIYWFIFTAAVAYHOPT-----L 475
Db 531 PLH--VAAKYGSIDVAKLLIQRRRAADSAGKNGLTFL-----HYAAHNDQNKVALLL 581
QY 476 KKOAAPIHLKAEVGNLSMLTGH 497
Db 582 EKGASPHATKNGTGPL--HI 600

```

US-09-112-096-15

```

: Sequence 15, Application us/09112096
: Patent No. 6194152
: GENERAL INFORMATION:
: APPLICANT: Reinert Laus
: APPLICANT: Michael H. Shapiro
: APPLICANT: Larissa Tsavalet
: TITLE OF INVENTION: Prostate Tumor Polynucleotide and
: FILE OF INVENTION: Antigen Compositions
: FILE REFERENCE: 7636-0015.30
: CURRENT APPLICATION NUMBER: US/09/112,096
: CURRENT FILING DATE: 1998-07-09
: EARLIER APPLICATION NUMBER: 60/056,110
: EARLIER FILING DATE: 1997-08-20
: NUMBER OF SEQ ID NOS: 29
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 15
: LENGTH: 1095
: TYPE: PRT
: ORGANISM: Homo sapiens
: US-09-112-096-15

```


GenCore version 4.5
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OM protein - protein search, using sw model.

Run on: October 3, 2001, 17:34:07 ; Search time 11.96 Seconds
(without alignments)
2360.077 Million cell updates/sec

Title: US-09-445-614-2

Perfect score: 4376
Sequence: 1 MTSPPSSPVRLLETLDDGGE.....EDEDGASENYPVOLLQSN 824

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 93435 segs, 34255486 residues

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	215	4.9	973	1	TRP5_HUMAN
2	198.5	4.5	1275	1	TRP6_MOUSE
3	197.5	4.5	1124	1	TRP1_DROME
4	153.5	3.5	809	1	TRP1_MOUSE
5	151	3.5	3924	1	ANK2_HUMAN
6	150.5	3.4	793	1	TRP1_HUMAN
7	145	3.3	1964	1	TRP4_MOUSE
8	140	3.2	1862	1	ANK1_MOUSE
9	139	3.2	848	1	TRP3_HUMAN
10	138	3.2	1880	1	ANK1_HUMAN
11	134	3.1	178	1	CHHC_BOMMO
12	133.5	3.1	642	1	VA2A_SCHPO
13	130.5	3.0	212	1	AGT1_WHEAT
14	130	3.0	930	1	TRP6_MOUSE
15	129.5	3.0	1246	1	TMV2_CAEEL
16	129	2.9	806	1	PA26_HUMAN
17	129	2.9	2715	1	PA26_HUMAN
18	128.5	2.9	169	1	KRUA_HUMAN
19	128.5	2.9	2703	1	NOTC_DROME
20	126	2.9	212	1	AGT1_HORVU
21	124.5	2.8	124	1	CHH2_BOMMO
22	124.5	2.8	186	1	AGI3_WHEAT
23	123.5	2.8	213	1	AGI3_WHEAT
24	123	2.8	581	1	TRR_RAT
25	123	2.8	2871	1	FBN1_HUMAN
26	122.5	2.8	277	1	J11_HGMVA
27	122.5	2.8	3075	1	LMAL_HUMAN
28	121.5	2.8	182	1	KRUC_SHEEP
29	121.5	2.8	194	1	KRUC_HUMAN
30	121.5	2.8	1503	1	TRP7_HUMAN
31	121	2.8	2871	1	FBN1_BOVIN
32	120.5	2.8	823	1	YNS2_CAEEL
33	119.5	2.7	357	1	SH5A_RAT

34	119	2.7	836	1	TRP3_MOUSE	09qzcl mus musculu
35	119	2.7	931	1	TRP6_HUMAN	09y210 homo sapien
36	118.5	2.7	105	1	MT1_TERRI	P80394 tetrahymena
37	118.5	2.7	657	1	RES2_SCHPO	P41412 schizosacch
38	117.5	2.7	633	1	YSV1_CAEEL	Q22566 caenorhabd1
39	116	2.7	357	1	5H5A_MOUSE	P30966 mus musculu
40	116	2.7	3712	1	LM1_PARP	P17053 parametium
41	116	2.7	3712	1	LM1_DROME	000174 drosophila
42	115.5	2.6	2444	1	NTC1_HUMAN	P46531 homo sapien
43	115	2.6	1401	1	LAT1_LATMA	P23631 latrodectus
44	114	2.6	1093	1	SW14_YEAST	P25302 saccharomyc
45	113.5	2.6	2531	1	NTC1_RAT	007008 rattus norv

ALIGNMENTS

RESULT	ID	TRP5_HUMAN	STANDARD	PRT	973 AA.
AC	09UL62				
DT	01-OCT-2000	(rel. 40, Created)			
DT	01-OCT-2000	(rel. 40, Last sequence update)			
DT	01-OCT-2000	(rel. 40, Last annotation update)			
DE	TRANSIENT RECEPTOR POTENTIAL CHANNEL 5 (HTRP-5).				
GN	TRP5 OR TRP5.				
OS	Homo sapiens (Human)				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.				
ON	NCBI_Taxid=9606;				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=Brain;				
RX	MEDLINE=94425273; PubMed=10493832;				
RA	Sossey-Alaoui K., Lyon J.A., Jones L., Abidi F.E., Hartung A.J.,				
RA	Hane B., Schwartz C.E., Stevenson R.E., Srivastava A.K.;				
RT	"Molecular cloning and characterization of TRP5 (HTRP5), the human				
RT	homologue of a mouse brain receptor-activated capacitative Ca(2+)				
RT	entry channel."				
RL	Genomics 60:330-340(1999).				
CC	-1- FUNCTION: SUGGESTED TO MEDIATE CAPACITATIVE CALCIUM ENTRY (CCE).				
CC	SEEMS TO FORM A CALCIUM PERMEANT CHANNEL.				
CC	-1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).				
CC	-1- SIMILARITY: BELONGS TO THE TRANSIENT RECEPTOR FAMILY.				
CC	-1- SIMILARITY: CONTRAINS 2 ANK REPEATS.				
CC	-----				
CC	THIS SWISS-PROT entry is copyright. It is produced through a collaboration				
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -				
CC	the European Bioinformatics Institute. There are no restrictions on its				
CC	use by non-profit institutions as long as its content is in no way				
CC	modified and this statement is not removed. Usage by and for commercial				
CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/				
CC	or send an email to license@sib-sib.ch).				
CC	-----				
CC	EMBL: AF054568; AAF00002.1; -				
DR	InterPro: IPR002110; -				
DR	InterPro: IPR002111; -				
DR	InterPro: IPR002153; -				
DR	Pfam: PF00023; ank; 2.				
DR	PRINTS: PR01097; TRANSPARENT.				
KW	Ionic channel; Transmembrane; Ion transport; Calcium channel;				
KW	ANK repeat; Repeat; Glycoprotein.				
FT	TRANSMEM 331 351				POTENTIAL.
FT	TRANSMEM 364 384				POTENTIAL.
FT	TRANSMEM 399 419				POTENTIAL.
FT	TRANSMEM 438 458				POTENTIAL.
FT	TRANSMEM 471 491				POTENTIAL.
FT	TRANSMEM 513 533				POTENTIAL.
FT	TRANSMEM 568 588				POTENTIAL.
FT	TRANSMEM 604 624				POTENTIAL.
FT	REPEAT 69 98				ANK 1.
FT	REPEAT 141 170				ANK 2.
FT	CARBOHYD 91 91				N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CAROHD 461 461 N-LINKED (GLCNAc. . .) (POTENTIAL).
 FT CAROHD 625 625 N-LINKED (GLCNAc. . .) (POTENTIAL).
 FT CAROHD 678 678 N-LINKED (GLCNAc. . .) (POTENTIAL).
 FT CAROHD 900 900 N-LINKED (GLCNAc. . .) (POTENTIAL).
 SQ SEQUENCE 973 AA; 111411 MW; FBC8CBF17BE42166 CRC64;

Query Match 4.9%; Score 215; DB 1; Length 973;
 Best Local Similarity 20.5%; Pred. No. 6.6e-07;
 Matches 162; Conservative 115; Mismatches 278; Indels 234; Gaps 36;

QY 182 KAVLN-LKDVAVACLPILQIDRDSGNPOPLVNAOCTDYTHGSHALHAIKRSLOQYK 240
 DB 34 KAPLAVENGDAVAKALQAEIYYN-VINCMPL-GRSALLAIENEMLEIME 87
 QY 241 LLEVNGANY-----HARACGREFKOGQGC-YPGEL----- 271
 DB 88 LLNHSVYVGDALLAIKREVYGVALLSYRPSG-EKQVPLMDTQSPETPDIT 144
 QY 272 PLSLACTKQMDVSYL-----NPHQASLQATDSOGNTVLAHVMSDMSAENIAL 325
 DB 145 PMLAAHTNNEYIKLVQKRVITPRPHQ-----IRNCVCEYS- 183
 QY 326 VASMTDGLQAGARCLPVOLEDINQDLPPLKLAKEGKTEIRHILQRFSGLSHS 385
 DB 184 -SSEVDLSHRSR-----LNIYKALSPSLALSSDEDPILTAER-LGWELKELSKYE 234
 QY 386 RKF-TEMCGPVRVSLYDASVSCSESVLEIIAF-----CK 423
 DB 235 NEFKAYEELSOQCKLFDKOLLDOARSRELEIILNHDSHEELDPOKYHDLAKVAI 294
 QY 424 SPHRHVVLEPLNKLQAKV----- 444
 DB 295 KYHOKEFAVQPCOOLLATIMFDGPPGRKRWVYKLTCTMTIGFLPMLSTAYLISPRS 354
 QY 445 -DLIPKFLNFCN-----LHYMFIPAVANH-QPLKQQAHLKAEVNSMLLGH 496
 DB 355 NGLTIKKPFIFCHTMSYLFELMLLASQHYRTDLHVOGPPRYVE--MWILPW- 410
 QY 497 ILLGGIYLVAGOLM-YFMRHVEWISFIDSEIFLFOALLTVVSOVLCFLAIE- 553
 DB 411 -VLGFIWGEIKEMMDGFEYIHDMMNMDFANSLY-LATISIKIYAVKNGS 463
 QY 554 -----WYPLYSAL-----VLGMLLYTTCFQHTGTYSMICQVILDLRL 600
 DB 464 RPREMEMHPTLAEALFAISNLSRLISLFTANSHLPLOLISLRML-DLKFLF 522
 QY 601 IYVLFQFVAVLVSQEAHREAPTPGNATESVQPMGEGDEGNGAYGILASDEL 660
 DB 523 IYCVLLAFANGLNOL-YFIYETRAIDEPNCKGIR--CEKONNA--FSTLETTLOSL 575
 QY 661 FKFTIGMEL-----AFEOQIHFHGVNLLLLAVLTYLLMLMLTALMSFVNSVAT 714
 DB 576 FMSVGLNLVYTVKKAHFEFEVGAT-MEGTVNLSVLLMLLMAANNNSQOLAD 633
 QY 715 DSMSTWKLQKA--ISVE-----HENGW--WCRKKORAGVMT 749
 DB 634 HADIEMKFARKLWMSYDEGGTLPPIIPSPKSFYLTGNWENNTCEPKRD----- 686
 QY 750 VQTKDGSPPDERWCFRVEVVMASW-EOTLPTICDPSGAGVPRTLNPLVLSPPKED- 807
 DB 687 ----PDGRRRR-----NLRSTERNADSLIONHOYOEYIRLVKRYVAAAMIRNSKT 734
 QY 808 -DGASEENY 815
 DB 735 HEGLTEENF 743

RESULT 2
 TRP_DROME STANDARD; PRT; 1275 AA.
 AC P19334;
 DT 01-NOV-1990 (Rel. 16, Created)

DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE TRANSIENT RECEPTOR POTENTIAL PROTEIN.
 CN TRP.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 CX NCBI_Taxid=7227;
 [1]
 RN SEQUENCE FROM N.A.
 RP STRAIN=OREGON-R;
 RC MEDLINE=90180449; PubMed=2516726;
 RX Montell C., Rubin G.M.;
 RA "Molecular characterization of the Drosophila trp locus: a putative
 RT integral membrane protein required for phototransduction.";
 RL Neuron 2:1313-1323(1989).
 [2]
 RN SEQUENCE FROM N.A.
 RP MEDLINE=90148782; PubMed=2482778;
 RX Wong F., Schaefer E.L., Roop B.C., Lamendola J.N., Johnson-Seaton D.,
 RA Shao D.;
 RT "Proper function of the Drosophila trp gene product during pupal
 RT development is important for normal visual transduction in the
 RT adult.";
 RL Neuron 3:81-94(1989).
 [3]
 RN SEQUENCE OF 1126-1275 FROM N.A.
 RP MEDLINE=88042982; PubMed=3118483;
 RX Wong F., Yuh Z.T., Schaefer E.L., Roop B.C., Ally A.H.;
 RA "Overlapping transcription units in the transient receptor potential
 RT locus of Drosophila melanogaster.";
 RL Somat. Cell Mol. Genet. 13:661-669(1987).
 CC -1- FUNCTION: REQUIRED FOR PHOTOTRANSDUCTION. SUGGESTED TO MEDIATE
 CC CALCIUM ENTRY. SEEMS TO FORM A LIGHT-SENSITIVE CALCIUM PERMEANT
 CC CHANNEL.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
 CC -1- TISSUE SPECIFICITY: EXPRESSED PREDOMINANTLY IN THE RHABDOMERIC
 CC MEMBRANES OF THE PHOTORECEPTOR CELLS.
 CC -1- SIMILARITY: BELONGS TO THE TRANSIENT RECEPTOR FAMILY.
 CC -1- SIMILARITY: CONTAINS 2 ANK REPEATS.
 CC
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 DR EMBL; M34394; AAA28976.1; -;
 DR EMBL; M21306; AAA56928.1; -;
 DR EMBL; M18634; AAA28977.1; -;
 DR PIR; J00092; J00092.
 DR PIR; J00015; J00015.
 DR FlyBase; FBgn0003861; trp.
 DR InterPro; IPR002110; -;
 DR InterPro; IPR002153; -;
 DR Pfam; PF00023; ank; 1.
 DR PRINTS; PR01097; TRNSRCEPTR.
 DR PROSITE; PS50088; ANK_REPEAT; 1.
 DR PROSITE; PS50297; ANK_REPEAT_REGION; 1.
 KW Ionic channel; Transmembrane; Ion transport; Calcium channel;
 KW Vision; ANK repeat; Repeat.
 FT TRANSMEM 334 354
 FT TRANSMEM 378 401
 FT TRANSMEM 419 436
 FT TRANSMEM 457 471
 FT TRANSMEM 504 527
 FT TRANSMEM 612 630
 FT TRANSMEM 636 661
 FT REPEAT 69 98
 FT REPEAT 143 172
 FT ANK 1.
 FT ANK 2.

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FT CONFLICT 285 288 GORO -> ASSE (IN REF. 2).
FT CONFLICT 326 329 RRQ -> POE (IN REF. 2).
FT CONFLICT 365 374 KPEVFTHS -> NPSSSTRTP (IN REF. 2).
FT CONFLICT 785 785 S -> N (IN REF. 2).
SQ SEQUENCE 1275 AA; 142589 MW; 91CPCDD989698B1 CRC64;

Query Match 4.5%; Score 198.5; DB 1; Length 1275;
Best Local Similarity 19.9%; Pred. No. 1.1e-05;
Matches 130; Conservative 100; Mismatches 251; Indels 171; Gaps 27;

OY 213 NAOCSTDYRGRSHALHIAIEKRSLOCVCLVENGANVHARACGRFGQGCFTFGLP 272
DB 62 NINOTDPNMR--SALISAENENEDLAVILEHNIEV-----GDALLHAISEXY 108
OY 273 LSLACTKQMDVSYLLENPHQSPASLQATDSQNTV---LHALVMSIDNSAENIALVTSM 329
DB 109 VEAVEBELLQWETNH---KEGQPSMEAVDSKSTFTYDITPLILAAHNNNEIILKI--- 162
OY 330 YDGLLQAGARL-----CPTVOLED-----IRNLQDLPPLKILAAKGGK 366
DB 163 ---LLDRGATLPMPHDVYKCGCECVTSQTDLSLRHSQRINAYRALSASLIALSSRPV 219
OY 367 IEIFRHILQREFSGLSHRSKFTENCYGPVAVSLYDAS--VDSCSENSVLEITAFCKS 424
DB 220 LTVFO--LSWELKRLQANSESEFRAE-YTEMROMQDFTGSLDHARTMELEVMNFNHE 276
OY 425 P-----HHRMAYLEP--LNKLLQAKWDLIPKF----- 451
DB 277 PSHNICLGQOTLERKLAIKRYKOTVAPHPNOQLAAIHWYDGLPGRKROASQOLMD 336
OY 452 FLNPLCNLIYFTFAVAYHQPTLKKQAPHLKAEVNSMELTGHILLIGIYLLVGL 511
DB 337 VVKLGCFPIYSLKYLAPDEGAKFMKRPVKFTHSCSTW--FELMLLGAASLRVQOI 394
OY 512 -----WYF-----WRRH-----VF-----I 521
DB 395 TFEELAPFMULTMEDMKHERGSLPGIELAITTYMALIFEELKSLYDGLFEYIMDL 454
OY 522 W--ISFIDSYFEILFLF--QALLTVSQCVCFLAIEWYL-----PLVVS-----A 562
DB 455 WNIYDYSNMYYVWILCRATAYIVHRDLMPFRGIDLPFPREHMHPPPMILISBAGFAG 514
OY 563 LVIGMLNLVYTRGFQHTGIYSVMIOKAVILRDLRFLLIYLVFEGFAVALVLSQEAMR 622
DB 515 MYFSYKLKLVHIFESINPHLGLOVSLGRMI-DIKKFFIYTVLVFAFG---CGNLQLLMY 570
OY 623 PEARTGNATESVQPMGQDEGNGA-----QYRGILEASLELKFRTIGMGLAQF--- 674
DB 571 -YALEEKNCYHLHPDVAEDDOEKACTIWRFSNLEFETSSQLFWASGCLVDLVSFDIAG 629
OY 675 -QLFRGMVILLILAYVLLTYILLNLMLALMSETVNSVARDMSIMKLOKA 725
DB 630 IKSTTRWALLMGSSYSVINITYVLLNLMLAMNSYQIISERADTEWKFARS 681

RESULT 3
TRPL_DROME STANDARD; PRT; 1124 AA.
AC P48994:
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE TRANSIENT-RECEPTOR-POTENTIAL LIKE PROTEIN.
GN TRPL.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephyrididae; Drosophilidae; Drosophila.
OX NCBI_Taxid=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=OREGON-R.

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RX MEDLINE-92232293; PubMed-1314616;
RA Phillips A.M., Bull A.L., Kelly L.E.;
RT "Identification of a Drosophila gene encoding a calmodulin-binding
protein with homology to the trp phototransduction gene.";
RL Neuron 8:631-642(1992)
CC -1- FUNCTION: BINDS CALMODULIN. SUGGESTED TO MEDIATE CALCIUM ENTRY.
CC -1- SEEMS TO FORM A LIGHT-SENSITIVE CALCIUM PERMEANT CHANNEL.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
CC -1- TISSUE SPECIFICITY: EXPRESSED PREDOMINANTLY IN THE RHABDOMERIC
CC -1- MEMBRANES OF THE PHOTORECEPTOR CELLS.
CC -1- SIMILARITY: BELONGS TO THE TRANSIENT RECEPTOR FAMILY.
CC -1- SIMILARITY: CONTAINS 2 ANK REPEATS.
CC -----
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CC -----
DR EMBL: M88185; AAA28979.1; -.
DR FlyBase: FBgn0005614; trpl.
DR InterPro: IPR002110; -.
DR InterPro: IPR002153; -.
DR Pfam: PF00023; ank; 2.
DR PRINTS: PR01097; TRANSRECEPT.
DR PROSITE: PS50088; ANK_REPEAT; 1.
DR PROSITE: PS50297; ANK_REPEAT_REGION; 1.
DR Kwd: Ionic channel; Transmembrane; Ion transport; Calcium channel;
KW Calmodulin-binding; Valsion; ANK repeat; Repeat.
FT TRANSMEM 341 361 POTENTIAL.
FT TRANSMEM 374 394 POTENTIAL.
FT TRANSMEM 432 452 POTENTIAL.
FT TRANSMEM 513 533 POTENTIAL.
FT TRANSMEM 549 569 POTENTIAL.
FT TRANSMEM 609 629 POTENTIAL.
FT TRANSMEM 646 666 POTENTIAL.
FT REPEAT 78 107 ANK 1.
FT REPEAT 152 181 ANK 2.
FT DOMAIN 710 727 CALMODULIN-BINDING (POTENTIAL).
FT DOMAIN 809 825 CALMODULIN-BINDING (POTENTIAL).
SQ SEQUENCE 1124 AA; 127697 MW; E14796D55A2C10BD CRC64;

Query Match 4.5%; Score 197.5; DB 1; Length 1124;
Best Local Similarity 19.7%; Pred. No. 1.1e-05;
Matches 162; Conservative 130; Mismatches 281; Indels 249; Gaps 38;

OY 191 VNACILPPLQIDRDSGNPOPL-----VNAOCTDD 219
DB 25 VGGCCVPL-----GLPOLLLEKFLAVRGDMPNVRRIQKALRHOHINICMDP 77
OY 220 YXRGSHALHIAIEKRSLOCVCLVENG-----ANVHARAC-----GRFPQK 261
DB 78 L--GRRAFLAIDNENLEMVLLVVGVEYKDALHLHNAEVEAVELLEHEELIKES 135
OY 262 Q-----GTCFYFGL-PLSLACTKQMDVSYLLEN-----PH-----QPSL 298
DB 136 EPIYMWOKYDINTAFADPITPLMLAAHNNNEILRIIDRGAAVVPVDRGCGECVRL 195
OY 299 QATDSQNTVLAH-----ALVMSIDNSAENIALVTSYDGLQAGARLCPVOLED 348
DB 196 TAEDSLRHSLSRVNIYRALCPSLICLSNDPSSATQVLSMELNLAITDECKSETMDL 255
OY 349 IRNLQ-----DITPLKLAKEGKIEI-----FRHILQREFSGLSHRSKFTENC 392
DB 256 RROCKFAVDLLDQTRINSNELAITINDPQMSYEPGDMSLTRLYVAISYKQKFFV--A 313
OY 393 YGPVAVSL-----YLLAVSDSCSENSVLEITAFCKSPRHRYAVLEPNKLL-----QAK 443
DB 314 HSNIOQLSSITWD--GLPGRRRSIVDKYI--CIA-----QVAVLFLYCLHYMCAPNCR 365

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OY 444 WDLIRKFLNLCN---LIMETITANA-----YHOPIKQOAPHLAENGN 489
DB 366 TQOLMKPKPMKFLIHASSYFLFLILVSOBADDFAVIFGTRMKELAEQELBQRCQ 425
OY 490 SMLTGHILLIGGIYLVGOLMYFRHVFIMISPIDSEFELFEQALL--TVYSQVL 547
DB 426 ----TPSKLELIVMYV----IGFWEEVQELFANQMSYLNMMWFIDPLNLSIVSW 477
OY 548 CELAIEW-----YLP-----LVSAVLGMLNLYYTRGFQ 578
DB 478 CLRAVAYIQATEIARDPQWAIYIPREKMHDPQQLAEGLFAANVFSALKLVHLESTNP 537
OY 579 HGITSVMOQYILNDLFLFLIYVLFGEFVALVLSQEM-----RPAAPGPNNAT 632
DB 538 HLGPIQDISGRMYI-DIVAFEFYLVYFAFA---CGLNQLMYAALKSKCYVLPF-- 591
OY 633 ESYQPMEGQDEGNGA-----OYRGILEASLELFKFTIGMGL-----AFQEDLHR 679
DB 592 -----GADWGSNODSCMKRRRGNLFESSQSIFWASFGVGLDDELGSIKYTRFW 644
OY 680 GAVLLLLAYVLLTYILLMLALMSETVNSVATDSWIMKLOKASVLENGYWCRC 739
DB 645 G--LMEFGSYVINYVLLNLLIAMSNSYAMIDEHSDTEMKFAR-----TKLMSX 694
OY 740 KQORAGVMTVGTCKPDGSDERMCERY-----DEVNANSEQLPTIC 782
DB 695 FDSA---TLPPFNVLPSEVWVIRIFRKSSTIDROSKRKKEQOESEYDINIRSLV 750
OY 783 EDPGAGVPRTLENPLVLAAPPKE--DGASENYVPVOLL 822
DB 751 W-RYVAAMHRKEN---NPVEDDINEYKSEINIMRYEMLE 767

RESULT 4
TRP1_MOUSE STANDARD: PR: 809 AA.
ID AC 061056: 035722:
DT 01-OCT-2000 (Rel. 40, Created)
DT 01-OCT-2000 (Rel. 40, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE TRANSIENT RECEPTOR POTENTIAL CHANNEL 1 (TRANSIENT RECEPTOR PROTEIN 1)
DE (TRP1) (TRP-RELATED PROTEIN 1)
GN TRP1 OR TRP1 OR TRP1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RN SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
RC TISSUE-Insulinoma; PubMed-9165220;
RX MEDLINE-97307994; PubMed-9165220;
RA Sakura H., Ashcroft F.M.;
RT Identification of four trp1 gene variants murine pancreatic beta-
RT cells";
RL Diabetologia 40:528-532(1997).
RN [2]
RN SEQUENCE FROM N.A. (BETA ISOFORM).
RC TISSUE-Lens epithelium;
RA Rae J.L.;
RT "Ion channels in lens epithelia";
RL Submitted (Oct-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RN SEQUENCE OF 551-615 FROM N.A.
RX MEDLINE-96234226; PubMed-8646775;
RA Zhu X., Jiang M., Boulay G., Hurst R., Stefani E.,
RA Birnbaumer L.;
RT "trp, a novel mammalian gene family essential for agonist-activated
RT capacitance Ca2+ entry.";
RL Cell 85:661-671(1996).
CC -1- FUNCTION: SUGGESTED TO MEDIATE CAPACITATIVE CALCIUM ENTRY (CCE).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS, ALPHA (SHOWN HERE) AND BETA; ARE

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CC PRODUCED BY ALTERNATIVE SPLICING.
CC -1- SIMILARITY: BELONGS TO THE TRANSIENT RECEPTOR FAMILY.
CC -1- SIMILARITY: CONTAINS 3 ANK REPEATS.
CC
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DR EMBL: U73625; AAB50622.1;
DR EMBL: U95167; AAC53162.1;
DR EMBL: AF191551; AAF05725.1;
DR EMBL: U40980; AAC52699.1;
DR MGD: MGI:109528; Trp1.
DR InterPro: IPR002111;
DR InterPro: IPR002153;
DR PRINTS: PR01097; TRNSRECEPTR.
KW Ionic channel; Transmembrane; Ion transport; Calcium channel;
KW ANK repeat; Repeat; Alternative splicing.
FT TRANSMEM 367
FT TRANSMEM 403
FT TRANSMEM 432
FT TRANSMEM 512
FT TRANSMEM 556
FT TRANSMEM 603
FT TRANSMEM 633
FT TRANSMEM 653
FT REPEAT 62
FT REPEAT 91
FT REPEAT 99
FT REPEAT 128
FT REPEAT 174
FT CARBOHYD 86
FT CARBOHYD 110
FT CARBOHYD 303
FT CARBOHYD 322
FT CARBOHYD 322
FT CARBOHYD 397
FT VARSPLIC 126
FT SEQUENCE 809 AA; 92727 MW; DFD8377DSC538CDD CRC64;
SQ
Query Match 3.5%; Score 153.5; DB 1; Length 809;
Best Local Similarity 18.8%; Pred. No. 0.0066;
Matches 137; Conservative 115; Mismatches 242; Indels 235; Gaps 33;
OY 158 LSKTSKYLTDSYETGSGTKLMKAY-----LNKDGYNAC-----ILPLQTD 202
DB 27 LSGVSSSLPSSPSSSPSSPNEVALKDREKENTLNKFLFLACDGDYVWKKILE-E 85
OY 203 RDSGNPOPLVNAOCTDYRGSHALHIAIEKRSLOCVKLVENGAN-----VHARAC 254
DB 86 NSSGD-----LNNCVD--VLGNNAVITITENSLLDILLDDYGGOSADALLVAIDSEV 139
OY 255 G-----RFFQKGGCGCTFGE-----LPLSACTKQMDVSYLLE--- 290
DB 140 GAVDLLNHRPRKRSRPTIVKLMERIONPEYSTMDVAPVILAAARNNEYILTMKKQV 199
OY 291 ---NPH-----QPSALQNTDSCGNTVLAALVMI 315
DB 200 SLPRHAVGCECTTCSANKKDSLRHSRFLDIYCLASPALIMLTER--DPLRAFELS 257
OY 316 SD-----NSAENIALVYSMYDGLLAGARLCTVQLEDIRN----- 351
DB 258 ADKLKSLVEVEFRNDYELARQCMKFKDLAQR--NSRRELYILNHTSSDEPLDKRG 315
OY 352 ---LQDITPLKLAKEKIEIFRHIILOPREGSLHSRKFTWCYGPVRSVLYLASVD 407
DB 316 LLEERMLNLSRLKLAIKYN-----QKEF-----VSQS 341
OY 408 SCEENSVETIAFHCKSPHRR-----MVYLE-----QAKWDLIRKF 451
DB 342 NCOQ--FLNTVWFGOMSGYRKRPCKTKIMVLTGIVFWPVLUSLCYLIAKPSQFRIHTP 399

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OY 452 FLNLCMLIMFT-----AVAYHPTLKQAAPHKAEVGSMLTGLLIGIT 505
DB 400 FMKIIIGASYFFELLNLNLSLVNEDK-----KNTMGALERIDYLLT- 445
OY 506 LVNGOLYFNRHAFIWFISFDSYFE-----ILFLQA--LLTYVSQVLCLEAI- 552
DB 446 WIIGMTSDIKR---LWYEGIEDFLESRNOLSFVMSLVATFALKVANKHDFADR 502
OY 553 -EW--YLPFLVSAVLGMLNLLYTRGFHTGISVW-----IQRVILRDLRFLLYLV 604
DB 503 KMDAHPRLVAEGLFANVLSTYLFPMYTTSSILGPIQISGMQDCKFLGMLL 562
OY 605 FLGFANALVLSLOEAMRPEAPGPNAATESYQPMEGDEGNGAIGILEASLEFRET 664
DB 563 VLFSTIGTLQYDKGY-----TSKEOKDCVGFCEQOSNDT---FHSFGTCFALFWYI 614
OY 665 IGMGELAF-----OEQJHFRGMVLLLLAYVLLTYILLNMLALMSTVSATDS 716
DB 615 FSLAHVAIFVTRSYGEBELQSFVGAV--IVGTYNVVVYVLTLLVAMLRKSFQLIANHE 672
OY 717 WSIMKLOKA 725
DB 673 DKEMKFA 681

RESULT 5
ANK2_HUMAN STANDARD: PRT: 3924 AA.
ID ANK2_HUMAN 001484; 001485;
AC 001484; 001485;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE ANKYRIN 2 (BRAIN ANKYRIN) (ANKYRIN B) (ANKYRIN, NONERYTHROID).
GN ANK2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN (1)
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE-Brain stem;
RX MEDLINE-94075409; PubMed-8253844;
RA Chan W., Kordeli E., Bennett V.;
RT 440-kD ankyrinB: structure of the major developmentally regulated
RT domain and selective localization in unmyelinated axons.";
RL J. Cell Biol. 123:1463-1473(1993).
RN (2)
RP SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3).
RC TISSUE-Brain stem;
RX MEDLINE-91302466; PubMed-1830053;
RA Otto E., Kunimoto M., McLaughlin T., Bennett V.;
RT Isolation and characterization of cDNAs encoding human brain
RT ankyrins reveal a family of alternatively spliced genes.";
RL J. Cell Biol. 114:241-253(1991).
RN (3)
RP REVISIONS.
RA Carpenter S.;
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
RN (4)
RP SEQUENCE OF 463-495 FROM N.A.
RX MEDLINE-92009921; PubMed-1833308;
RA Tse W.T., Menninger J.C., Yang-Feng T.L., Francke U., Sahr K.E.,
RA Lux S.E., Ward D.C., Forget B.G.;
RT Isolation and chromosomal localization of a novel nonerythroid
RT ankyrin gene";
RL Genomics 10:858-866(1991).
RN (5)
RP FUNCTION: ANKYRINS ATTACH INTEGRAL MEMBRANE PROTEINS TO CYTO-
RP SKELETAL ELEMENTS; THEY BIND TO THE ERYTHROCYTE MEMBRANE PROTEIN
RP BAND 4.2, TO NA-K ATPASE, TO THE LYMPHOCYTE MEMBRANE PROTEIN
RP AND TO THE CYTOSKELETAL PROTEINS FODRIN, TUBULIN, VIMENTIN AND
RP DESMIN. ERYTHROCYTE ANKYRINS ALSO LINK SPECTRIN (BETA CHAIN) TO
RP THE CYTOPLASMIC DOMAIN OF THE ERYTHROCYTES ANION EXCHANGE PROTEIN;
RP THEY RETAIN MOST OR ALL OF THESE BINDING FUNCTIONS.

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OY 316 SD-----NSAENIALVTSMYDGLLONARLCPVQLEDIRN----- 351
DB 242 ADLKEISLVEFRNRYEELARCKMFADLLAQAR--NSRELEVILNHTSSDEPLDRG 299
OY 352 ----LQDLTPKLAKAEKGIIEFRHILQREFSGLSHLSRKFTEMCVGPVAVSLDASVD 407
DB 300 LLEERNLNRKKAIAKYN-----QKEF-----VSQS 325
OY 408 SCEENSULTEIAFHCKSPHRR-----NVYLE-----PLNKL-----QAKMDLIPKF 451
DB 326 NCOQ--FLNTWEGQMSGYRRKPTCKIMTVLVGIFWPLSLCYLIAPRSQGRITHP 383
OY 452 FLNFCNLNLYMFIET-----AAVYHQPILKQAAPHLAEVNSMLIGHIILIGGIT 505
DB 384 FMKFIHGAASYFFELLNLLYSLYNEDK-----KNTMGPALERIDYLL----- 429
OY 506 LVLGOLMYFMRHVFHIFISFIDSYFE-----ILFLQA--LLTVASQVLCFLAI----- 552
DB 430 WITGMMSDIKR--LWYGLEDFLEESRNOISFVNSLILATFALKVVAHNKFHDPAIR 486
OY 553 -EM--YLPPLVSALVGMNLLYTRGFQHTGIYSVM-----IQVILDLRFLIYLV 604
DB 487 KQMDAFHPTLVAGELFAFANVLSYLRLFMYTSSILGLPIQISMGLQDFGKFLMELL 546
OY 605 FLFGFVALVSLSQEMAREAPRGPNATESVOPMEQDEBGNQAYRGILASLELFKFT 664
DB 547 VLFSTFGLTOLYDKGY-----TSKEQKDCVGIFCEQSDNDT---PHSFGTCFALFWYI 598
OY 665 IGMGELAF-----QEQLHFRGMVLLLLVYLLTYLLMLLALASEYNASVATDS 716
DB 599 FSLAHVAIVTFPSYGELOSFVGAV--IVGTYNVVVIVLTKLVAMLHKSPQLIANHE 656
OY 717 WSIWKLQKA 725
DB 657 DKEMKFAFA 665

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RL Development 122:2251-2259(1996).
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- DISEASE: ACTIVATED INT-3 TRANSFORMS MAMMARY EPITHELIAL CELLS.
CC -1- SIMILARITY: CONTAINS 29 EGF-LIKE DOMAINS.
CC -1- SIMILARITY: CONTAINS 5 ANK REPEATS.
CC -1- SIMILARITY: CONTAINS 5 ANK REPEATS.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DB EMBL: M80456; AAB38377.1; -
DB EMBL: U43691; AAC52630.1; -
DB PIR: A38072; TYWV73.
DB HSSP: P00740; IIXA.
DB MGD: MGI:107471; Notch4.
DB InterPro: IPR000152; -
DB InterPro: IPR000561; -
DB InterPro: IPR000800; -
DB InterPro: IPR001438; -
DB InterPro: IPR001881; -
DB InterPro: IPR002110; -
DB Pfam: PF00008; EGF; 27.
DB Pfam: PF00023; ank; 6.
DB Pfam: PF00066; notch; 2.
DB PRINTS: PR00010; EGFBLDOD.
DB PROSITE: PS50088; ANK_REPEAT; 5.
DB PROSITE: PS50297; ANK_REPEAT_REGION; 1.
DB PROSITE: PS00010; ASX_HYDROXYL; 11.
DB PROSITE: PS00022; EGF_1; 28.
DB PROSITE: PS01186; EGF_2; 21.
DB PROSITE: PS01187; EGF_CA; 9.
KW Differentiation; Neurogenesis; Repeat; EGF-like domain; Transmembrane;
KW Glycoprotein; Proto-oncogene; ANK repeat; Signal.
FT SIGNAL 1 20
FT CHAIN 1 21
FT TRANSMEM 21 144
FT TRANSMEM 144 144
FT DOMAIN 145 196
FT DOMAIN 21 60
FT DOMAIN 61 112
FT DOMAIN 115 152
FT DOMAIN 153 189
FT DOMAIN 191 229
FT DOMAIN 231 271
FT DOMAIN 273 309
FT DOMAIN 311 350
FT DOMAIN 352 388
FT DOMAIN 389 427
FT DOMAIN 429 470
FT DOMAIN 472 508
FT DOMAIN 510 546
FT DOMAIN 548 584
FT DOMAIN 586 622
FT DOMAIN 622 656
FT DOMAIN 658 686
FT DOMAIN 688 724
FT DOMAIN 726 762
FT DOMAIN 764 800
FT DOMAIN 803 839
FT DOMAIN 841 877
FT DOMAIN 878 924
FT DOMAIN 926 962
FT DOMAIN 964 1000
FT DOMAIN 1002 1040
FT DOMAIN 1042 1081
FT DOMAIN 1083 1122
FT DOMAIN 1126 1167
FT REPEAT 1168 1208

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FT	REPEAT	1209	1242	LIN/NOTCH 2.
FT <td>REPEAT</td> <td>1209</td> <td>1242</td> <td>LIN/NOTCH 2.</td>	REPEAT	1209	1242	LIN/NOTCH 2.
FT <td>REPEAT</td> <td>1243</td> <td>1282</td> <td>LIN/NOTCH 3.</td>	REPEAT	1243	1282	LIN/NOTCH 3.
FT <td>REPEAT</td> <td>1628</td> <td>1657</td> <td>ANK 1.</td>	REPEAT	1628	1657	ANK 1.
FT <td>REPEAT</td> <td>1661</td> <td>1691</td> <td>ANK 2.</td>	REPEAT	1661	1691	ANK 2.
FT <td>REPEAT</td> <td>1695</td> <td>1724</td> <td>ANK 3.</td>	REPEAT	1695	1724	ANK 3.
FT <td>REPEAT</td> <td>1728</td> <td>1757</td> <td>ANK 4.</td>	REPEAT	1728	1757	ANK 4.
FT <td>REPEAT</td> <td>1761</td> <td>1790</td> <td>ANK 5.</td>	REPEAT	1761	1790	ANK 5.
FT <td>DISULFID</td> <td>25</td> <td>38</td> <td>BY SIMILARITY.</td>	DISULFID	25	38	BY SIMILARITY.
FT <td>DISULFID</td> <td>32</td> <td>48</td> <td>BY SIMILARITY.</td>	DISULFID	32	48	BY SIMILARITY.
FT <td>DISULFID</td> <td>50</td> <td>59</td> <td>BY SIMILARITY.</td>	DISULFID	50	59	BY SIMILARITY.
FT <td>DISULFID</td> <td>65</td> <td>77</td> <td>BY SIMILARITY.</td>	DISULFID	65	77	BY SIMILARITY.
FT <td>DISULFID</td> <td>71</td> <td>100</td> <td>BY SIMILARITY.</td>	DISULFID	71	100	BY SIMILARITY.
FT <td>DISULFID</td> <td>102</td> <td>111</td> <td>BY SIMILARITY.</td>	DISULFID	102	111	BY SIMILARITY.
FT <td>DISULFID</td> <td>119</td> <td>130</td> <td>BY SIMILARITY.</td>	DISULFID	119	130	BY SIMILARITY.
FT <td>DISULFID</td> <td>124</td> <td>140</td> <td>BY SIMILARITY.</td>	DISULFID	124	140	BY SIMILARITY.
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FT <td>DISULFID</td> <td>157</td> <td>168</td> <td>BY SIMILARITY.</td>	DISULFID	157	168	BY SIMILARITY.
FT <td>DISULFID</td> <td>162</td> <td>177</td> <td>BY SIMILARITY.</td>	DISULFID	162	177	BY SIMILARITY.
FT <td>DISULFID</td> <td>179</td> <td>188</td> <td>BY SIMILARITY.</td>	DISULFID	179	188	BY SIMILARITY.
FT <td>DISULFID</td> <td>195</td> <td>208</td> <td>BY SIMILARITY.</td>	DISULFID	195	208	BY SIMILARITY.
FT <td>DISULFID</td> <td>202</td> <td>217</td> <td>BY SIMILARITY.</td>	DISULFID	202	217	BY SIMILARITY.
FT <td>DISULFID</td> <td>219</td> <td>228</td> <td>BY SIMILARITY.</td>	DISULFID	219	228	BY SIMILARITY.
FT <td>DISULFID</td> <td>235</td> <td>246</td> <td>BY SIMILARITY.</td>	DISULFID	235	246	BY SIMILARITY.
FT <td>DISULFID</td> <td>240</td> <td>259</td> <td>BY SIMILARITY.</td>	DISULFID	240	259	BY SIMILARITY.
FT <td>DISULFID</td> <td>261</td> <td>270</td> <td>BY SIMILARITY.</td>	DISULFID	261	270	BY SIMILARITY.
FT <td>DISULFID</td> <td>277</td> <td>288</td> <td>BY SIMILARITY.</td>	DISULFID	277	288	BY SIMILARITY.
FT <td>DISULFID</td> <td>282</td> <td>297</td> <td>BY SIMILARITY.</td>	DISULFID	282	297	BY SIMILARITY.
FT <td>DISULFID</td> <td>299</td> <td>308</td> <td>BY SIMILARITY.</td>	DISULFID	299	308	BY SIMILARITY.
FT <td>DISULFID</td> <td>315</td> <td>329</td> <td>BY SIMILARITY.</td>	DISULFID	315	329	BY SIMILARITY.
FT <td>DISULFID</td> <td>323</td> <td>338</td> <td>BY SIMILARITY.</td>	DISULFID	323	338	BY SIMILARITY.
FT <td>DISULFID</td> <td>340</td> <td>349</td> <td>BY SIMILARITY.</td>	DISULFID	340	349	BY SIMILARITY.
FT <td>DISULFID</td> <td>356</td> <td>367</td> <td>BY SIMILARITY.</td>	DISULFID	356	367	BY SIMILARITY.
FT <td>DISULFID</td> <td>361</td> <td>376</td> <td>BY SIMILARITY.</td>	DISULFID	361	376	BY SIMILARITY.
FT <td>DISULFID</td> <td>378</td> <td>387</td> <td>BY SIMILARITY.</td>	DISULFID	378	387	BY SIMILARITY.
FT <td>DISULFID</td> <td>393</td> <td>404</td> <td>BY SIMILARITY.</td>	DISULFID	393	404	BY SIMILARITY.
FT <td>DISULFID</td> <td>398</td> <td>415</td> <td>BY SIMILARITY.</td>	DISULFID	398	415	BY SIMILARITY.
FT <td>DISULFID</td> <td>417</td> <td>426</td> <td>BY SIMILARITY.</td>	DISULFID	417	426	BY SIMILARITY.
FT <td>DISULFID</td> <td>433</td> <td>449</td> <td>BY SIMILARITY.</td>	DISULFID	433	449	BY SIMILARITY.
FT <td>DISULFID</td> <td>443</td> <td>458</td> <td>BY SIMILARITY.</td>	DISULFID	443	458	BY SIMILARITY.
FT <td>DISULFID</td> <td>460</td> <td>469</td> <td>BY SIMILARITY.</td>	DISULFID	460	469	BY SIMILARITY.
FT <td>DISULFID</td> <td>476</td> <td>487</td> <td>BY SIMILARITY.</td>	DISULFID	476	487	BY SIMILARITY.
FT <td>DISULFID</td> <td>481</td> <td>496</td> <td>BY SIMILARITY.</td>	DISULFID	481	496	BY SIMILARITY.
FT <td>DISULFID</td> <td>498</td> <td>507</td> <td>BY SIMILARITY.</td>	DISULFID	498	507	BY SIMILARITY.
FT <td>DISULFID</td> <td>514</td> <td>525</td> <td>BY SIMILARITY.</td>	DISULFID	514	525	BY SIMILARITY.
FT <td>DISULFID</td> <td>519</td> <td>534</td> <td>BY SIMILARITY.</td>	DISULFID	519	534	BY SIMILARITY.
FT <td>DISULFID</td> <td>536</td> <td>545</td> <td>BY SIMILARITY.</td>	DISULFID	536	545	BY SIMILARITY.
FT <td>DISULFID</td> <td>552</td> <td>563</td> <td>BY SIMILARITY.</td>	DISULFID	552	563	BY SIMILARITY.
FT <td>DISULFID</td> <td>557</td> <td>572</td> <td>BY SIMILARITY.</td>	DISULFID	557	572	BY SIMILARITY.
FT <td>DISULFID</td> <td>574</td> <td>583</td> <td>BY SIMILARITY.</td>	DISULFID	574	583	BY SIMILARITY.
FT <td>DISULFID</td> <td>590</td> <td>601</td> <td>BY SIMILARITY.</td>	DISULFID	590	601	BY SIMILARITY.
FT <td>DISULFID</td> <td>595</td> <td>610</td> <td>BY SIMILARITY.</td>	DISULFID	595	610	BY SIMILARITY.
FT <td>DISULFID</td> <td>612</td> <td>621</td> <td>BY SIMILARITY.</td>	DISULFID	612	621	BY SIMILARITY.
FT <td>DISULFID</td> <td>626</td> <td>637</td> <td>BY SIMILARITY.</td>	DISULFID	626	637	BY SIMILARITY.
FT <td>DISULFID</td> <td>631</td> <td>646</td> <td>BY SIMILARITY.</td>	DISULFID	631	646	BY SIMILARITY.
FT <td>DISULFID</td> <td>648</td> <td>655</td> <td>BY SIMILARITY.</td>	DISULFID	648	655	BY SIMILARITY.
FT <td>DISULFID</td> <td>662</td> <td>669</td> <td>BY SIMILARITY.</td>	DISULFID	662	669	BY SIMILARITY.
FT <td>DISULFID</td> <td>664</td> <td>674</td> <td>BY SIMILARITY.</td>	DISULFID	664	674	BY SIMILARITY.
FT <td>DISULFID</td> <td>676</td> <td>685</td> <td>BY SIMILARITY.</td>	DISULFID	676	685	BY SIMILARITY.
FT <td>DISULFID</td> <td>692</td> <td>703</td> <td>BY SIMILARITY.</td>	DISULFID	692	703	BY SIMILARITY.
FT <td>DISULFID</td> <td>697</td> <td>712</td> <td>BY SIMILARITY.</td>	DISULFID	697	712	BY SIMILARITY.
FT <td>DISULFID</td> <td>714</td> <td>723</td> <td>BY SIMILARITY.</td>	DISULFID	714	723	BY SIMILARITY.
FT <td>DISULFID</td> <td>723</td> <td>741</td> <td>BY SIMILARITY.</td>	DISULFID	723	741	BY SIMILARITY.
FT <td>DISULFID</td> <td>730</td> <td>750</td> <td>BY SIMILARITY.</td>	DISULFID	730	750	BY SIMILARITY.
FT <td>DISULFID</td> <td>735</td> <td>751</td> <td>BY SIMILARITY.</td>	DISULFID	735	751	BY SIMILARITY.
FT <td>DISULFID</td> <td>752</td> <td>761</td> <td>BY SIMILARITY.</td>	DISULFID	752	761	BY SIMILARITY.
FT <td>DISULFID</td> <td>768</td> <td>779</td> <td>BY SIMILARITY.</td>	DISULFID	768	779	BY SIMILARITY.
FT <td>DISULFID</td> <td>773</td> <td>788</td> <td>BY SIMILARITY.</td>	DISULFID	773	788	BY SIMILARITY.
FT <td>DISULFID</td> <td>790</td> <td>799</td> <td>BY SIMILARITY.</td>	DISULFID	790	799	BY SIMILARITY.
FT <td>DISULFID</td> <td>807</td> <td>818</td> <td>BY SIMILARITY.</td>	DISULFID	807	818	BY SIMILARITY.
FT <td>DISULFID</td> <td>812</td> <td>827</td> <td>BY SIMILARITY.</td>	DISULFID	812	827	BY SIMILARITY.
FT <td>DISULFID</td> <td>829</td> <td>838</td> <td>BY SIMILARITY.</td>	DISULFID	829	838	BY SIMILARITY.
FT <td>DISULFID</td> <td>845</td> <td>856</td> <td>BY SIMILARITY.</td>	DISULFID	845	856	BY SIMILARITY.
FT <td>DISULFID</td> <td>850</td> <td>865</td> <td>BY SIMILARITY.</td>	DISULFID	850	865	BY SIMILARITY.
FT <td>DISULFID</td> <td>867</td> <td>876</td> <td>BY SIMILARITY.</td>	DISULFID	867	876	BY SIMILARITY.

CC ELEMENTS: BIND TO THE ERYTHROCYTE MEMBRANE PROTEIN BAND 4.2, TO
 CC NA-K APPAS, TO THE LYMPHOCYTE MEMBRANE PROTEIN GP85, AND TO THE
 CC CYTOSKELETAL PROTEINS FODRIN, TUBULIN, VIMENTIN AND DESMIN.
 CC ERYTHROCYTE ANKIRINS ALSO LINK SPECTRIN (BETA CHAIN) TO THE
 CC CYTOPLASMIC DOMAIN OF THE ERYTHROCYTE ANION EXCHANGE PROTEIN;
 CC THEY RETAIN MOST OR ALL OF THESE BINDING FUNCTIONS.
 CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC SURFACE OF ERYTHROCYTIC
 CC PLASMA MEMBRANE.
 CC -1- PTM: REGULATED BY PHOSPHORYLATION (BY SIMILARITY).
 CC -1- PTM: ACYLATED BY PALMITIC ACID GROUP(S) (BY SIMILARITY).
 CC -1- SIMILARITY: CONTAINS 23 ANK REPEATS.
 CC -----
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 CC -----
 CC EMBL: M84756; AAA37236.1; -
 CC DR HSSP: Q00420; IAWC.
 CC DR MGD: MGI:88024; Ank1.
 CC DR InterPro: IPR000488; -
 CC DR InterPro: IPR000906; -
 CC DR InterPro: IPR002110; -
 CC DR Pfam: PF00791; 205; 1.
 CC DR Pfam: PF00023; ank; 23.
 CC DR Pfam: PF00531; death; 1.
 CC DR PROSITE: PS50088; ANK_REPEAT: 20.
 CC DR PROSITE: PS50297; ANK_REGION: 1.
 CC DR PROSITE: PS50017; DEATH_DOMAIN: 1.
 CC DR Cytoskeleton; Repeat; ANK repeat; Phosphorylation; Lipoprotein.
 CC KW DOMAIN 1 827
 CC FT 828 1386
 CC FT 1387 1862
 CC FT DOMAIN 1862
 CC FT 40 69
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 CC FT REPEAT 106 135 ANK 3.
 CC FT REPEAT 139 168 ANK 4.
 CC FT REPEAT 170 197 ANK 5.
 CC FT REPEAT 201 230 ANK 6.
 CC FT REPEAT 234 263 ANK 7.
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 CC FT REPEAT 300 329 ANK 9.
 CC FT REPEAT 333 362 ANK 10.
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 CC FT REPEAT 399 428 ANK 12.
 CC FT REPEAT 432 461 ANK 13.
 CC FT REPEAT 465 494 ANK 14.
 CC FT REPEAT 498 527 ANK 15.
 CC FT REPEAT 531 560 ANK 16.
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 CC FT REPEAT 597 626 ANK 18.
 CC FT REPEAT 630 659 ANK 19.
 CC FT REPEAT 663 692 ANK 20.
 CC FT REPEAT 696 725 ANK 21.
 CC FT REPEAT 729 758 ANK 22.
 CC FT REPEAT 762 791 ANK 23.
 CC FT REPEAT 794 827 ANK 24.
 CC FT DOMAIN 1862
 CC FT 1862 AA; 204242 MW; AEB85B5B29001E5 CRC64;
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 CC Query Match 3.28; Score 140; DB 1; Length 1862;
 CC Best Local Similarity 24.08; Pred. No. 0.13;
 CC Matches 74; Conservative 37; Mismatches 109; Indels 88; Gaps 12;
 CC 223 GHSALTAIERKSLQCVLTVENGVNANV-----HARACGRFFQKG--Q 262
 CC | : |||| : : : ||| : ||| :
 CC | : |||| : : : ||| : ||| :

Db 367 GTPPLIATCKNNHIRMWELLKTGASIDAVTESGLTPPLHVASFWGHPIVKNLLRGASP 426
 QY 263 GTCYFEGELPLSLAACQKMDVSYLLENPHOPASQATOSQGVTVLHVMDSNSEN 322
 Db 427 NWSVAKVETPLHMAARGHVEVAKYLLQNKAK-RANAAKDQ--TPHICARIGH----- 478
 QY 323 IALVTSMYDGLQAGARLCTPTVQLEDIRNQLDPLPLKIAKEKIEFFRIIILREFSGLS 382
 Db 479 ----TGWVKLLLENGAS-----PNIATAGHTPLPHTAREGHVDALALLKEASQAC 527
 QY 383 HLSKRTFEM---CYGVRVSLVDLASVDSCENSVLEITAFHCKSPHRRMYVLEPL-- 436
 Db 528 MTRKGFPLHVAARYKGVRLA-----ELLEHDAPHNAAGKNGPLPLHV 571
 QY 437 ----NKLQAKMPLDLPKFFLNFLCNLIYFIFTAVAYHQPILKQAAPLKA-----EY 487
 Db 572 AVHNNNDIVK--LLPLR-----GSSPHSPANNGYTPLHIAKQNOIEV 613
 QY 488 GN\$MLLTG 495
 Db 614 ARSLLOYG 621
 RESULT 9
 ID TRP3_HUMAN STANDARD; PRT: 848 AA.
 AC 013507; O00593; 015660;
 DT 01-OCT-2000 (Rel. 40, Created)
 DT 01-OCT-2000 (Rel. 40, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE TRANSIENT RECEPTOR POTENTIAL CHANNEL 3 (TRP-3).
 GN TRP3 OR TRP3.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_Taxid:9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE:96234226; PubMed:8646775;
 RA Zhu X., Jiang M., Peyton M., Boulay G., Hurst R., Stefani E.,
 RA Birnbaumer L.;
 RT *trp, a novel mammalian gene family essential for agonist-activated
 RT capacitative Ca2+ entry.";
 RL Cell 85:661-671(1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE:97358541; PubMed:9215637;
 RA Xu X.-Z.S., Li H.-S., Guggino W.B., Montell C.;
 RT "Coassembly of TRP and TRPL produces a distinct store-operated
 RT conductance.";
 RL Cell 89:1155-1164(1997).
 RN [3]
 RP SEQUENCE OF 632-747 FROM N.A.
 RC TISSUE-Brain;
 RX MEDLINE:96003837; PubMed:7568191;
 RA Wes P.D., Chevesich J., Jeromin A., Rosenberg C., Stetten G.,
 RA Montell C.;
 RT "TRPC1, a human homolog of a Drosophila store-operated channel.";
 RL Proc. Natl. Acad. Sci. U.S.A. 92:9652-9656(1995).
 CC -1- FUNCTION: SUGGESTED TO MEDIATE CAPACITATIVE CALCIUM ENTRY (CCE).
 CC SEEMS TO FORM A CALCIUM PERMEANT CHANNEL.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
 CC -1- SIMILARITY: BELONGS TO THE TRANSIENT RECEPTOR FAMILY.
 CC -1- SIMILARITY: CONTAINS 4 ANK REPEATS.
 CC -----
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 CC -----

DR EMBL: U47050; AAC51653.1; -
 DR EMBL: Y13758; CAA/4083.1; -
 DR EMBL: X89068; CAA61448.1; -
 DR MIM: 602345; -
 DR InterPro: IPR002110; -
 DR InterPro: IPR002111; -
 DR InterPro: IPR002153; -
 DR Pfam: PF00023; ank; 2.
 DR PRINTS: PR01097; TRANSRECEPT.
 KW Ionic channel; Transmembrane; Ion transport; Calcium channel;
 FT TRANSMEM 350
 FT TRANSMEM 370
 FT TRANSMEM 382
 FT TRANSMEM 402
 FT TRANSMEM 431
 FT TRANSMEM 451
 FT TRANSMEM 464
 FT TRANSMEM 484
 FT TRANSMEM 536
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 FT REPEAT 73
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 FT CONFLICT 739
 FT CONFLICT 742
 SO SEQUENCE 848 AA; 97354 MW; 1DBC92BC941DE416 CRC64;

Query Match 3.2%; Score 139; DB 1; Length 848;
 Best Local Similarity 18.4%; Pred. No. 0.064;
 Matches 128; Conservative 96; Mismatches 222; Indels 248; Gaps 32;

OY 212 VNAOCTDDYRGHSALHIEKRSLOCVKLV--ENGANY-----HAR----- 252
 DB 65 LVNVCVD--YMGOMALQLVGNHLEVTBLKREMLNIGALLLAISKGYRIVEAIL 122
 OY 253 -----ACGRFEFGK-----OGTCFYEGLPLSLACTKOMPVSYLL-- 289
 DB 123 NHPGFAKRLTSPCEQLODDDFYVDEDTGRSPDITPIILAHCKQKYEVMHLMK 182
 OY 290 -----ENPH-----OPASIQATDSOGNTVLAHY 313
 DB 183 GARIEPHDYFCCKDCMEKORHDSFSHSRINAYKGLASAVYLSL--SSSDPYLTAL 240
 OY 314 MISDSAEVIALVTSMD-----GLLAGARLC--PYVLEDIRN--LQDL 355
 DB 241 L--SHEMLAKLANIEKFNKYRKLSMOCKDFYVGVLD--LCRDSEEEALINDLES 294
 OY 356 TPLKLAKEGKIEFRH--ILQREFSGLSLSRKFTFW--CYGPVRSYLDIASVSC 411
 DB 295 EFL-----EVHRKASLSRVKLAITYEVKKFVAHPNCCOQLITTYE--NISGLRE 343
 OY 412 NSVLELIAHCKSPRRHRVVL-----EPLNKLQAKWDLIPKFEFL 453
 DB 344 -----QTIAIKC-----LVVLVVALGLPELAIGYWIAPCSLGLILNSP-----FM 384
 OY 454 NFLCNLIYFIFTAVAYHO-----PLKQAAPHKLAEGNSMLTGLLIL-- 500
 DB 385 KVVAAHASFILFLGLLVFNASDRFEGITTLPIKITVTDYRKQIFRKTKQFTWEMLIW 444
 OY 501 -LGSIILVGLQLMY-----FMRHVEI-----WISF-----IDSY 529
 DB 445 VLGMMSEKELMBSGPREYIIQLMNVDFGLMSTIFIAFTKFLAFLQATRAQOYVSY 504
 OY 530 FIFLFLQALLTVVSQVLCFLAIEWYLP-----LLVSALVGLWNLNLYTGRFOHT 580
 DB 505 VQESDLSEVTLPEPIQYFYARDKW-LPSDDQIISEGLYALVAVLSFSRIAILLRANSEF 563
 OY 581 GIYSWIAQVILRLDLRLILLYLVLFGEPAVALVLSQEAHPPEAPTCGNPNATESVQPM 640

DB 564 GPELOISIGRTY-KDIFKEFVFLIMVFAFMIGMFLYSYLGAKV----- 607
 OY 641 QDEEGGAGYRGLLEASLELFKFTIMGELA-----FQQLFRGMVLLLLAYVL 691
 DB 608 -----NAAFTVESEKTLFWSIFGLSEVTSVLYKDHKFTENIGY-----VLGIYVY 656
 OY 692 LTVIILLNMLIALMSETVNSVATDSWIKLOKA 725
 DB 657 TAVVILLNMLIMINSYOEIEDDSVEKFKARS 690

RESULT 10
 ANK1_HUMAN
 ID ANK1_HUMAN STANDARD; PRT; 1880 AA.
 AC P16157;
 DT 01-APR-1990 (Rel. 14, Created)
 DT 01-APR-1990 (Rel. 14, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE ANKYRIN 1 (ERYTHROCYTE ANKYRIN) (ANKYRIN R) (ANKYRINS 2.1 AND 2.2).
 GN ANK1 OR ANK.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 OC NCBI_TaxID=9606;
 [1]
 SEQUENCE FROM N. A., PARTIAL SEQUENCE, AND VARIANTS.
 TISSUE=Hematopoietic;
 MEDLINE=9015830; PubMed=2137557;
 Lux S.E., John K.M., Bennett V.;
 "Analysis of cDNA for human erythrocyte ankyrin indicates a repeated structure with homology to tissue-differentiation and cell-cycle control proteins.";
 Nature 344:36-42(1990).
 [2]
 SEQUENCE FROM N. A.
 MEDLINE=90175370; PubMed=1689849;
 Lambert S., Yu H., Prychal J.T., Lawler J., Ruff P., Speicher D.,
 Cheung M.C., Kan Y.W., Palek J.;
 "cDNA sequence for human erythrocyte ankyrin.";
 Proc. Natl. Acad. Sci. U.S.A. 87:1730-1734(1990).
 [3]
 VARIANT HS IIE-462.
 MEDLINE=96225450; PubMed=8640229;
 Eber S.W., Gonzalez J.M., Lux M.L., Scarpa A.L., Tse W.T.,
 Downwell M., Herbers J., Kugler W., Gezcan R., Pekrun A.,
 Gallagher P.G., Schroeter W., Forget B.G., Lux S.E.;
 "Ankyrin-1 mutations are a major cause of dominant and recessive hereditary spherocytosis.";
 Nat. Genet. 13:214-218(1996).
 -1- FUNCTION: ANKYRIN INTEGRAL MEMBRANE PROTEIN TO CYTOSKELETAL ELEMENTS; BIND TO THE ERYTHROCYTE MEMBRANE PROTEIN BAND 4.2, TO NA-K ATPASE, TO THE LYMPHOCYTE MEMBRANE PROTEIN GP85, AND TO THE CYTOSKELETAL PROTEINS FODRIN, TUBULIN, VIMENTIN AND DESMIN. ERYTHROCYTE ANKYRINS ALSO LINK SPECTRIN (BETA CHAIN) TO THE CYTOSKELETAL DOMAIN OF THE ERYTHROCYTES ANION EXCHANGE PROTEIN; THEY RETAIN MOST OR ALL OF THESE BINDING FUNCTIONS.
 -1- SUBCELLULAR LOCATION: CYTOPLASMIC SURFACE OF ERYTHROCYTIC PLASMA MEMBRANE.
 -1- ALTERNATIVE PRODUCTS: VARIOUS ISOFORMS OF ANKYRIN ARE PRODUCED BY ALTERNATIVE SPLICING. THE SEQUENCE SHOWN IS THAT OF ANKYRIN VARIANT 2.1.
 -1- PTM: REGULATED BY PHOSPHORYLATION.
 -1- PTM: ACYLATED BY PALMITIC ACID GROUP(S).
 -1- DISEASE: DEFECTS IN ANK1 ARE THE CAUSE OF DOMINANT AND RECESSIVE HEREDITARY SPHEROCYTOSIS (HS).
 -1- SIMILARITY: CONTAINS 23 ANK REPEATS.
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CC -----

DR EMBL; X16609; CA34610.1; -

DR EMBL; M28880; AAA51732.1; -

DR PIR; S08275; SJHUK.

DR PIR; A35049; A35049.

DR HSSP; 000420; 1AMC.

DR MIM; 182900; -

DR Interpro; IPR000488; -

DR Interpro; IPR000906; -

DR Interpro; IPR002110; -

DR Pfam; PF00791; ZU5; 1.

DR Pfam; PF00023; ank; 22.

DR Pfam; PF00531; death; 1.

DR PROSITE; PS50088; ANK_REPEAT; 20.

DR PROSITE; PS50297; ANK_REPEAT_REGION; 1.

DR PROSITE; PS50017; DEATH_DOMAIN; 1.

DR Cytoskeleton; Alternative splicing; Repeat; ANK repeat;

DR Phosphorylation; Lipoprotein; Multigene family; Disease mutation;

KM Elliptocytosis; Polymorphism.

FT INT_MET 0 826

FT DOMAIN 1

FT 827 1381

FT 1382 1880

FT 43 72

FT REPEAT 76 105

FT REPEAT 109 138

FT REPEAT 142 171

FT REPEAT 173 200

FT REPEAT 204 233

FT REPEAT 237 266

FT REPEAT 270 299

FT REPEAT 303 332

FT REPEAT 336 365

FT REPEAT 369 398

FT REPEAT 402 431

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FT REPEAT

DR InterPro: IPR02635; -
 Pfam: PF01723; Chorton; 1.
 KW Eggshell; Chorton; Repeat; Multigene family; Signal.
 FT SIGNAL 1 21
 FT CHAIN 22 178
 CHORION CLASS HIGH-CYSTEINE HCB PROTEIN
 FT DOMAIN 22 46
 FT DOMAIN 47 110
 FT DOMAIN 111 178
 SO SEQUENCE 178 AA; 16077 MW; 8AF703E0F65D3096 CRC64;

Query Match 3.1%; Score 134; DB 1; Length 178;
 Best Local Similarity 42.2%; Pred. No. 0.025;
 Matches 27; Conservative 0; Mismatches 31; Indels 6; Gaps 3;

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 DB 117 GCGGCGGCGG 174
 OY 142 CGAC 145
 DB 175 CGCC 178

RESULT 12

YA2A_SCHPO STANDARD; PRT; 642 AA.
 AC 009701;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE HYPOPHETICAL 72.5 KDA PROTEIN C2F7.10 IN CHROMOSOME 1.
 GN SPAC27.10.
 OS Schizosaccharomyces pombe (fission yeast).
 OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
 OC Schizosaccharomycetales; Schizosaccharomycetaceae;
 OC Schizosaccharomyces.
 OX NCBI_TaxID=4896;
 RN [1]
 RP SEQUENCE FROM N.A.

RC STRAIN=972;
 RA Gantles S., Churcher C.M., Barrell B.G., Rajandream M.A., Walsh S.V.;
 RL Submitted (JUL-1995) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: TO YEAST AKRI.
 CC -1- SIMILARITY: CONTAINS 6 ANK REPEATS.

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CC EMBL: 250143; CAA90497.1; -
 DR HSSP: Q00420; IAWC.
 DR InterPro: IPR001594; -
 DR InterPro: IPR002110; -
 DR Pfam: PF00023; ank; 6.
 DR Pfam: PF01529; zf-DHHC; 1.
 DR PROSITE: PS50086; ANK_REPEAT; 3.
 DR PROSITE: PS50297; ANK_REPEAT_REGION; 1.
 KW Hypothetical Protein; ANK repeat; Repeat.
 FT REPEAT 1 29
 FT REPEAT 33 62
 FT REPEAT 67 96
 FT REPEAT 100 129
 FT REPEAT 133 162
 FT REPEAT 166 196
 SO SEQUENCE 642 AA; 72521 MW; C83584A3300BDAD0 CRC64;

Query Match 3.1%; Score 133.5; DB 1; Length 642;
 Best Local Similarity 21.0%; Pred. No. 0.11;
 Matches 95; Conservative 71; Mismatches 136; Indels 151; Gaps 23;

OY 212 VNACTDDYRGRSHALHAIEKRSLQCVKLTVENGANYHANACGRFQGGGTCTFPGEL 271
 DB 25 IDVATDE--GGATRLHMAALNQPICKFLEHGADVNAIG-----GDL 67
 OY 272 --PLSLAACKQMDVVSYLEENPHQASLQATDSQGTVALHVMISD----- 317
 DB 68 QAAPIHMAAKRGSVKTVHVLQHGADPL--LKDQGFNCFLHVAHASPILVYLHL 124
 OY 318 -----NSAENIALVTSNMG-----LLOAGARLCTVPLEDIRNODITPLKLAKE 364
 DB 125 ISVDLRDDQOHTPLMWSYHGENEPTNCLLMGADVALTDE-----DKMTPLHWSYVG 177
 OY 365 GKIEIFRHILQREFSGL-----SHLSRKF--TEHCY--GPVAVS--LYDLASVS--CBEN 412
 DB 178 GNLCMKMLIKE--GIPCTAVTANLSGQKTPALASLAVSHLFOALISNGLKVET 235
 OY 413 SVEETIAFHCKSPHRHNVVLEPLNKLQAKMDLIPKFLNPLCNLYMFTFAVAYHQ 472
 DB 236 SE-----EP-----EKWVAVPSKFPQSQTETIFCFL----- 262
 OY 473 PTLKKAAPHKAEGVSNMLTGHIILG-----GIYLVQGLM--YFWR----- 517
 DB 263 -----SSFTITGVFFIMSGICPWSILHAPLWYFTFKYITTCIHANI 306
 OY 518 ---HFVWISFIDSYFELLFLE---QALLVVSQVLCFLAEWFLPLVSLVGLWNL 571
 DB 307 DIHFVLETFPLAGISFIFVWCHSLIVPRTLPKPLSLLEVLISFTGIG----L 362
 OY 572 YTRGFQHTG---IYSVM-----IQRYILNDL 595
 DB 363 YVTRAFQNPQVYDVGAVQVQREIRSKLDKDL 395

RESULT 13

AGIL_WHEAT STANDARD; PRT; 212 AA.
 ID AGIL_WHEAT
 AC P10968;
 DT 01-JUL-1989 (Rel. 11, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 01-JUN-1994 (Rel. 29, Last annotation update)
 DE AGGLUTININ ISOLECTIN I PRECURSOR (WGA1) (ISOLECTIN A).
 OS Triticum aestivum (Wheat).
 OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
 OC Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae; Triticeae;
 OC Triticum.
 OX NCBI_TaxID=4565;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-91370843; PubMed-2491677;
 RA Smith J.J., Raikhel N.V.;
 RT "Nucleotide sequences of cDNA clones encoding wheat germ agglutinin
 RT isolectins A and D";
 RL Plant Mol. Biol. 13:601-603(1989).
 RP SEQUENCE OF 27-197.
 RC TISSUE=germ.
 RX MEDLINE-89279931; PubMed-2499688;
 RA Wright C.S., Raikhel N.V.;
 RT "Sequence variability in three wheat germ agglutinin isolectins:
 RT products of multiple genes in polyploid wheat";
 RL J. Mol. Evol. 28:327-336(1989).
 RN [3]
 RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
 RX MEDLINE-91039324; PubMed-2231724;
 RA Wright C.S.;
 RT "2.2-A resolution structure analysis of two refined
 RT N-acetylneuramyl-lactose-wheat germ agglutinin isolectin
 RT complexes";
 RL J. Mol. Biol. 215:635-651(1990).

RA Bues M., Engler O., Hirsch H.H., Moroni C.;
 RT "Search for oncogenic regulators in an autocrine tumor model using
 RT differential display PCR: Identification of novel candidate genes
 RT including the calcium channel mtrp6.";
 RL Oncogene 18:1487-1494(1999).
 RN [3]
 RP SEQUENCE OF 631-739 FROM N.A.
 RC TISSUE-Brain;
 RX MEDLINE-9623426; PubMed-8646775;
 RA Zhu X., Jiang M., Peyton M., Boulay G., Hurst R., Stefani E.,
 RA Birnbaumer L.;
 RT "trp, a novel mammalian gene family essential for agonist-activated
 RT capacitative Ca2+ entry.";
 RL Cell 85:661-671(1996).
 CC -1- FUNCTION: NONSELECTIVE CAPACITATIVE CALCIUM ENTRY CHANNEL SUBUNIT.
 CC MEDIATES CALCIUM ENTRY STIMULATED BY A G-PROTEIN COUPLED RECEPTOR.
 CC BUT NOT BY INTRACELLULAR CALCIUM STORE DEPLETION. ACTIVATED BY
 CC DIACYLGLYCEROL (DAG) IN A MEMBRANE-DELIMITED FASHION INDEPENDENTLY
 CC OF PROTEIN KINASE C. IT IS PERMEABLE FOR CALCIUM, CESIUM, SODIUM,
 CC POTASSIUM AND MAGNESIUM.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
 CC -1- TISSUE SPECIFICITY: LUNG AND BRAIN.
 CC -1- PTM: N-GLYCOSYLATED.
 CC -1- SIMILARITY: BELONGS TO THE TRANSIENT RECEPTOR FAMILY.
 CC -1- SIMILARITY: CONTAINS 3 ANK REPEATS.
 CC -----
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 CC -----
 DR EMBL: U49069; AAC06146.1; -
 DR EMBL: AF057748; AAC64394.1; -
 DR MGD: MGI:109523; Trp6.
 DR InterPro: IPR002110; -
 DR InterPro: IPR002153; -
 DR Pfam: PF00023; ank; 2.
 DR PRINTS: PR01097; TRNSRECEPT.
 DR PROSITE: PSS0088; ANK_REPEAT_1.
 DR PROSITE: PSS0297; ANK_REPEAT_REGION_1.
 KW Ionic channel; Transmembrane; Ion transport; Calcium channel;
 KW ANK repeat; Repeat; Glycoprotein.
 KW -----
 FT TRANSMEM 406 426 POTENTIAL.
 FT TRANSMEM 438 458 POTENTIAL.
 FT TRANSMEM 487 507 POTENTIAL.
 FT TRANSMEM 521 541 POTENTIAL.
 FT TRANSMEM 592 612 POTENTIAL.
 FT TRANSMEM 636 656 POTENTIAL.
 FT TRANSMEM 706 726 POTENTIAL.
 FT REPEAT 131 160 ANK 1.
 FT REPEAT 162 188 ANK 2.
 FT REPEAT 217 246 ANK 3.
 FT CARBOHYD 26 26 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 361 361 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 393 393 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 560 560 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 616 616 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 727 727 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CONFLICT 3 56 MISSING (IN REF. 2).
 FT CONFLICT 103 103 V -> A (IN REF. 2).
 FT CONFLICT 114 114 W -> R (IN REF. 2).
 FT CONFLICT 134 134 N -> D (IN REF. 2).
 FT CONFLICT 184 184 S -> A (IN REF. 2).
 FT CONFLICT 371 371 D -> Y (IN REF. 2).
 FT CONFLICT 436 437 PR -> RG (IN REF. 2).
 FT CONFLICT 905 905 S -> T (IN REF. 2).
 FT SEQUENCE 930 AA; 106732 MW; CF21A426972732F3 CRC64;

Query Match

3.0%; Score 130; DB 1; Length 930;

Best Local Similarity 17.8%; Pred. No. 0.28;
 Matches 124; Conservative 98; Mismatches 220; Indels 254; Gaps 29;

QY 212 VNACCTDDYRGKSHALHAIEKRSLQCKLYL--ENGANV-----HARACGRF- 257
 DB 123 LNVACVD--YMGNAQLAVANEHELEITELLKKENSRVGDALLAISRYIVAEYL 180
 QY 258 ---FQKQ-----GTCFEGEPLSLAACKTQMDVVSYL- 289
 DB 181 NHPSFAGKRLATSPSQSELOQDDFYAVDEGCTRFSDVPTIIIAHQCEYEIHTLLRK 240
 QY 290 ---ENH-----QPSLQATDSOGTVLHALV 313
 DB 241 GARLERHDYFCCKTECSOKOKHDSFHSRSRINAYGLASPAVLSL--SSEDEVTAL 298
 QY 314 MISD-----NSAENIAL-VYSMDGLQAARIC-PRVQLEDIRN----- 351
 DB 299 LSNELAVLANIEKFKNDYRKLRSQCKDFVGLD---LCRNTVEEVALINGDAETROP 354
 QY 352 ---LQDLPPLKLAKEGKIEIFRH-----ILQREFSGLSLRSKFTWCYGPVRV 398
 DB 355 GDRGRPLSLKLAIKQEVKKFVAHPCCQQLSLIWEINLSGLRQGTMAKVELVLAVAL 414
 QY 399 SLVDLASVDSCEENSVLEIIAFHCKSPHRRMVVLEPLNKLQAKMDLLIPKFLNPLCN 458
 DB 415 GLPFLALIVWCAPCS-----KMGKILPRPMPKFAH 445
 QY 459 LIIMFTTAAVAYQPTLKKQAAPHLKAEGV-----NSMLLGHILILIGIYLL 507
 DB 446 AASFTEPLGLVNAADREFGKILLPNETSTDNAKOLFRRKTSQFSQSMEMLI---ISWV 501
 QY 508 VGOLM---YFW---RRHFIMISFIDSYEILFLQALLTVQVLCF----- 549
 DB 502 IGMIMAECKEIKWOGPREYIFELNMMD--FGMLATPA--SFLARMAAWHMSKASDII 557
 QY 550 -----LAIEW--YLPLVS-----ALVGLMNLLYYTRFQ 578
 DB 558 DANDTLKDLTKVTLGDNVKKYNNLARIKMDPTDQIISEGVLVAIVLFSRIAYILPANE 617
 QY 579 HTGIYSVMIOKVLRLDLRFLLIYVLFPGFAVALVLSQEAHPREPPTGPNATESQPM 638
 DB 618 SFPPLQISLGRIV-KDIFKVMVIFIMVFAFMIGMFLNLSYV-----IAKONEATTV 670
 QY 639 EGOEDGNGAQYIGLIEASLEFKFTIGMEL-----AFQDLHPFGVLLLLAY 689
 DB 671 E-----ESFTFLWAFGLSEVSVYINNHKFTENIGY-----VLGYV 710
 QY 690 VLLTYILLNMLIALMSETVNSVATDSWISWKLQRA 725
 DB 711 NYTMVIVLLNMLIAMINSFQIEDDADVEMKPARA 746
 RESULT 15
 YMW2_CAEEL
 ID YMW2_CAEEL STANDARD; PRT; 1246 AA.
 AC P34504; P34505; P34506; P90907;
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DE 30-MAY-2000 (Rel. 39, Last annotation update)
 DE HYPOTHETICAL 130.6 KDA PROTEIN K04H4.2 IN CHROMOSOME III.
 GN K04H4.2
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidae;
 OC Rhabditidae; Pelodierinae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2;
 RX MEDLINE-94150718; PubMed-7906398;
 RA Wilson R., Alnough R., Anderson K., Baynes C., Berks M.,
 RA Bonfield J., Burton J., Connell M., Copsy J., Coulson A.,
 RA Craxton M., Dear S., Du Z., Durbin R., Favell A., Fraser A.,
 RA Fulton L., Gardner A., Green P., Hawkins T., Hillier L., Jier M.,

RA Johnston L., Jones M., Kershaw J., Kirsten J., Laisster N.,
RA Latreille P., Lightning J., Lloyd C., Mortimore B., O'Callaghan M.,
RA Parsons J., Percy C., Rifkin A., Roopra A., Saunders D., Shownkeen R.,
RA Sims M., Smalton N., Smith A., Smith M., Sonnhammer E., Staden R.,
RA Sulston J., Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K.,
RA Waterson R., Watson A., Weinstock L., Wilkinson-Sproat J.,
RA Wohlman P.;
RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
RT elegans";
RL Nature 368:32-38(1994).
RN [2]
RP REVISIONS.
RC STRAIN-BRISTOL N2;
RA Durbin R.;
RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
CC K04H4.2B; ARE PROBABLY PRODUCED BY ALTERNATIVE SPLICING.
CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS; K04H4.2A (SHOWN HERE) AND
CC -1- SIMILARITY: TO CHITIN-BINDING MOTIFS.
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CC -----
DR EMBL; 227078; CAAB1587.1; -;
DR EMBL; 227078; CAAB1588.1; -;
DR PIR; S40992; S40992.
DR PIR; S40993; S40993.
DR PIR; S40994; S40994.
DR HSSP; P10966; IWGC.
DR WormPep; K04H4.2A; CEI19967.
DR WormPep; K04H4.2B; CEI19968.
KW Hypothetical protein; Alternative splicing.
FT VARSPLIC 166 529
FT IPTPTRTTEPPKRLCLSSNTDEVNSLGGASSSSATCGGTN
FT ANCTSEDECPPTKCYGGCKLAVCPRLSLTAVKTKQYH
FT CRANEHCFEGCCPKPTIELAVIKSOVLTKSKDNEHTKETEK
FT LIIGCEVDTRVKKCDIDICPEMSECVGICCKQPPKARC
FT NGMLALSIPVHCSDDCPIASRCYEGKCCPFLSESADST
FT SDSVGETTPVILKEEIIISTATKVKVKVDKISGVINKKCL
FT STQRCDLHLCPDFTCSLGGCKLNHCPCDGTVPETSCQ
FT SASNDHCPSSSHKCTLLNKEHFACCPSPGVVGVSTAEV
FT SECPIGSVEDPREFGTCRYSLQCPSPYFCNQRGQ -> Q
FT (IN ISOFORM K04H4.2B).
FT DSDTNTTNPSPQPTTKNTKNSKKHKKPKKKDVP
FT LSDPLLDNDFFPGPGYGPPEHLNLDLVLIRAGGECPPA
FT GLHCDTAINLCCPLLLPLADPNPKARKTKRRKQKODGNEM
FT EASANFPDSDPARFSSYSCGCMG -> VG (IN
FT ISOFORM K04H4.2B).
FT VARSPLIC 570 715
FT DSDTNTTNPSPQPTTKNTKNSKKHKKPKKKDVP
FT LSDPLLDNDFFPGPGYGPPEHLNLDLVLIRAGGECPPA
FT GLHCDTAINLCCPLLLPLADPNPKARKTKRRKQKODGNEM
FT EASANFPDSDPARFSSYSCGCMG -> VG (IN
FT ISOFORM K04H4.2B).
SQ SEQUENCE 1246 AA; 130610 MW; 4FA1A17D3F9606C4 CRC64;

Query Match 3.08; Score 129.5; DB 1; Length 1246;
Best Local Similarity 22.1%; Pred. No. 0.42;
Matches 64; Conservative 20; Mismatches 90; Indels 115; Gaps 15;
QY 81 NAVSRGVPG--AGGATCT-----GGCTGGACTT-----C 107
DB 784 NAVGACMSGRCSGYTCSNNVCCPQTITTFVCPDGTQAGGCVNGQCGTGYTCSNGLC 843
QY 108 CAGAGT-----AC-----CTGAGC-----AAGACCAG--CAAGTACCTCAC--GA 144
DB 844 CAGTSTTVKCLDGSDAVGACIPSCDGGGVQVSYCGSYCTTGTGNCPCPINSCPNGG 903
QY 145 CTCGEDLAGL-PEYLSKTSKYLTDEYTGSTGCTCLMKAVL---NLKGVNACILPLLO 200
DB 904 EVLGPITINGLCPTGYTVQGNLCCSATCTDGTGLPSVNGVCIDGYSLTNGV-CCPASVTC 962
QY 201 IDRDSCNPQPLVNAOCTDDYYRGHSALHTAIEKRSIQCVKL----- 241
DB 963 TDEISGP-----CTGTGFGNGGCPAGYACDSNQVNCPPVRYTDESCQVPAIDGLCP 1015

Oy 242 -----LVENGANVHARACGRFFQKGQGTCTCFYFGELPLSLAAC 278
Db 1016 PGYVVVYIPNSPLITNGVN-----PGTCI-----DLQCTTGLC 1048

Search completed: October 3, 2001, 17:37:37
Job time: 210 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: October 3, 2001, 17:32:07 ; Search time 21.54 Seconds
(Without alignments)
2914.013 Million cell updates/sec

Title: US-09-445-614-2

Sequence: 1 MTSFSSSFVRLLETLDGQE.....EDEDGASENYPVQLQSN 824

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

Database :
1: PIR1:
2: PIR2:
3: PIR3:
4: PIR4:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	1618	37.0	838	T09054	capsaicin receptor
2	634	14.5	725	JC7531	calcium transport
3	403.5	9.2	900	T33026	hypothetical prote
4	381.5	8.7	790	T20312	hypothetical prote
5	364	8.3	937	T37241	olfactory channel
6	261	6.0	519	T24772	hypothetical prote
7	200.5	4.6	1188	T19552	hypothetical prote
8	197.5	4.5	1124	JH0586	calmodulin-binding
9	191	4.4	1274	JN0015	trp protein - fruit
10	190.5	4.4	1275	JN0092	trp protein - fruit
11	169.5	3.9	810	T38361	trp protein - hu
12	157.5	3.6	481	T23729	hypothetical prote
13	157	3.6	1549	T13940	ankyrin - fruit fl
14	154	3.5	934	H71274	probable ankyrin -
15	151	3.5	1765	T42715	ankyrin 3, splice
16	151	3.5	1940	T42715	ankyrin 3, splice
17	151	3.5	1943	T42715	ankyrin 3, splice
18	151	3.5	1961	T42716	ankyrin 3, splice
19	151	3.5	3924	S37431	ankyrin 2, neurona
20	150.5	3.4	793	S68238	trp-1 protein - hu
21	150	3.4	887	T03939	potassium channel
22	150	3.4	4377	A55575	ankyrin 3, long sp
23	146	3.3	1964	T09059	notch4 - mouse
24	142.5	3.3	1435	T32930	hypothetical prote
25	140	3.2	1848	S37771	ankyrin, erythrocy
26	139.5	3.2	1862	T49502	ankyrin - mouse
27	139.5	3.2	1411	S30355	alpha-latroinsecto
28	138.5	3.2	223	B38346	ultra-high-sulfur
29	138	3.2	1856	B35049	ankyrin 1, erythro

30	138	3.2	1880	A35049	ankyrin 1, erythro
31	138	3.2	1881	SJHUK	ankyrin 1, erythro
32	137.5	3.1	164	T24272	hypothetical prote
33	135.5	3.1	230	A38346	ultra-high-sulfur
34	135	3.1	828	JC5807	trp3 protein - rat
35	134	3.1	178	A23219	high-cysteine chor
36	133.5	3.1	642	S58154	hypothetical prote
37	133	3.0	143	B21761	high cysteine chor
38	133	3.0	842	T32258	hypothetical prote
39	132.5	3.0	683	A85044	hypothetical prote
40	132.5	3.0	2703	A24420	hypothetical prote
41	132	3.0	791	T42691	notch protein - it
42	132	3.0	1001	S30385	hypothetical prote
43	132	3.0	1398	T21884	G9a protein - huma
44	131.5	3.0	598	D71127	hypothetical prote
45	131	3.0	616	T00894	hypothetical prote

ALIGNMENTS

RESULT 1
T09054
capsaicin receptor - rat
N:Alternate names: vanilloid receptor subtype 1
C:Species: Rattus norvegicus (Norway rat)
C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
C:Accession: T09054
R:Caeterina, M.J.; Schumacher, M.A.; Tomlinaga, M.; Rosen, T.A.; Levine, J.D.; Julius, Nature 389, 816-824, 1997
A:Title: The capsaicin receptor: A heat-activated ion channel in the pain pathway.
A:Reference number: 216539; PMID:98007969
A:Accession: T09054
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-838 <CAT>
A:Cross-References: EMBL:AF029310; NID:g2570932; PIDN:AAC53398.1; PID:g2570933
A:Experimental source: dorsal root ganglion
C:Keywords: ion channel; receptor

Query Match	37.0%	Score 1618;	DB 2;	Length 838;
Best Local Similarity	43.1%	Pred. No. 3.9e-108;		
Matches 360;	Conservative 128;	Mismatches 228;	Indels 120;	Gaps 17;
QY 18	GGEDGSEADRGKLDGSGGLPMESEFGEDRKFAPOIRVN---	LNVRKGTG-----	65	
DB 51	GGDSEAS-----	PLDCPEEGLASCPIITVSVLTIQRPDGPASVPSQ	99	
QY 66	---ASQDPNRFDRLEFNAYSRGVPGAGATCGGCTGGACTCCAGACTGAGC	121		
DB 100	DSVSGEKPRFLYDRSRITDAVAQ-----	123		
QY 122	AAGACGACCACTACCTCAGCTCGEDLAGLPEYLSTSKYLLDSEYTEGSGTKTCLM	181		
DB 124	-----SNC-----	QELSELPLDGRSKRLDSEKDETKTCLL	159	
QY 182	KAVLVKDGVAACIPLQLIDRSGNPOPVNAAGCTDYRRGSHALAIKRSIQCYKL	241		
DB 160	KAMLVHNGQNDTIALLDVARKTDSLKQFNASTDSYKQGTALHAIERRNLTVTL	219		
QY 242	LVENGANYHARACGRFPQGGG--TCFYFGEPLSLAACKQMDVSYLLENPHQPAISQA	300		
DB 220	LVENADADVQAANGDFEKKTKGRPGFYFGEPLSLAACKTNDLAIVKFLQNSWQPADISA	279		
QY 301	TDSQNTVLAHLMVMSDSANIALVTSMDGLIQAGARLCPTVOLIEDIRNLQDTPPLK	360		
DB 280	RDSVNTVLAHLMVEADVADVTMDTKFTSMYNEILLIGAKLHPITLKEITIRKGLTFLAL	339		
QY 361	AAKEKIEIFRIILQREF--SGLSLRSKRTFEMWCGPVRVSLYDLASVDSCEMSVLEIT	418		
DB 340	AASSGKIGVLAVIILQREIHEPECRLSRKRTFEMWVPHSSLYDLSCIDTEKNSVLEVI	399		

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0Y 419 AF-HKSHSRHMYVLEPILNKLKAKWLLPK-PELNFILCMLYLFETLAAYHQPLK 476
Db 400 AYSSETENRHDMLVEPLNRLLODKMDPEVKRIYENFNYCYLMIIFTLAAYRPV- 457
QY 477 KOAAP-HLKAEGVNSMLTGHILLGIGIYLLVGQLYFWRRHVFIMISFIDSEYELF 534
Db 458 -EGLEPPYKLKNTVGVYFVNTGELLISVSGGYEFFRGIDYFLQRRRSLSLFPDYSIELF 516
QY 535 LFOALLIVYSOYLCLEIAEWITPLVLSALVGLMNLITYTRGFQHTGIYSWAIQAVIIRD 594
Db 517 FVOSLEFMYAVSVLYFSQKREYVASVYFSLAGWIMLTYTRGFQOMGIIYAVIEMIIRD 576
QY 595 LLRFLLIYVLEFGAVNLVLSIOBAMRPEAPTGNNATESVOPMGQDEGGA----- 648
Db 577 LCREFEYVLELFEFSTVAVTILIED-----GKN--NSLPMESTPHKCRGSAKCRGN 625
QY 649 QYRGILEASLELFEKTIGMGEIAPQEOBLHFRGMVLLILLAVLYLTYILLNMLTAMSET 708
Db 626 SYNSLYSTCELEKFTICIMGDLFEFENDPKAVFIILLAYVILTYILLNMLTAMSET 685
QY 709 VNSVATDSWSTWLOKALISYLEMENGWYWC-RKKORAGVMLTVGTRKPDGSPDERMCFEVE 767
Db 686 VNKIAOESKNWTKLORAITIIDLTESFPLCKCRKKFRSCKLLQVGTPTPGDKDYYRWCFEVD 745
QY 768 EVNNAWSQETPLTCEDPGSA-GVPRTLNENPVLASPPREDDGSASEENYVYVQLIQ 822
Db 746 EVNNTTNTNTVGLINEDPGNCEGVAKTILSFELRSG---RVSGRWKKFALVPLLR 797

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RESULT      2
JC7531
calcium transport protein, Cat1 - human
C:Species: Homo sapiens (man)
C:Date: 31-Mar-2001 #sequence_revision 31-Mar-2001 #text_change 31-Mar-2001
C:Accession: JC7531
R:Peng, J.B.; Chen, X.; Berger, U.V.; Wieremowicz, S.; Morton, C.C.; Vassiliev, P.M.; Brown, Blochem. Biophys. Res. Commun. 276, 326-332, 2000
A:Title: Human calcium transport protein Cat1.
A:Reference number: JC7531; MUID:20551480
A:Accession: JC7531
A:Molecule type: mRNA
A:Residues: 1-725 <PEN>
A:Cross-references: CB:AF304463
C:Comment: This protein, a member of a family of Ca2+ channels, has a role in cellular cline and kidney.
C:Genetics:
A:Gene: Cat1
A:Map position: 7q33-34
C:Keywords: calcium channel; calcium transport; intestine; kidney; transport protein; th

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[illegible][illegible]

RESULT 3
T33026
hypothetical protein T09A12.3 - *Caenorhabditis elegans*
C:Species: *Caenorhabditis elegans*
C:Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
C:Accession: T33026
R:Hawkins, J.; Fulton, B.; Gillam, B.
submitted to the EMBL Data Library, February 1998
A:Description: The sequence of C. elegans cosmid T09A12.
A:Reference number: Z21265
A:Accession: T33026
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-900 <HAM>
A:Cross-references: EMBL:AF047660; PIDN:AA04431.1; GSPDB:GN00022; CESP:T09A12.3
A:Experimental source: strain Bristol N2; clone T09A12
C:Genetics:
A:Gene: CESP:T09A12.3
A:Map position: 4
A:Introns: 43/2; 86/3; 260/2; 396/3; 424/2; 495/1; 517/3; 553/3; 691/3; 741/3; 780/3;

	Query Match	9.2%	Score 403.5;	DB 2;	Length 900;	
	Best Local Similarity	24.1%	Pred. 0.5;e-21;			
	Matches 173;	Conservative 111;	Mismatches 241;	Indels 193;	Gaps 29;	
QY	158 LSKTSKYL-----TDSEYTE-----GSTKTKLMAKVNLAKGVNACILPILQI	201				
Db	122 LKKALKLLDGGGKGGRNSKYREISWKLKEERSMGEITIIGCCLLASDIHNLVLRIDY	181				
QY	202 DRDSGNPOLVNAACTDDYYRGSHALHAIEKRSLQCVKLVLENGANVHARCGRFF--	258				
Db	182 -----YPLRLNDIHISEDFY-GLSPLHQAIIINTDOCKLYYKFELKLGADVNSRCYGAFPCMD	235				
QY	259 -QKGGGT-----CFYFGELPLSLAACTKOMDVSYLLENPHOPASIQ	299				
Db	236 DOKSRFSDLSHEYEVELSLKTNYTGMMVLGEPFLPSFACLNOPESFRLLMEKANP---N	292				
QY	300 ATDSOGNTVEHALVNIWSNSAEINIALVTSMYDGILLQOAGARLCPTQOLEDIRLQDTPLK	359				
Db	293 AQTNGNSVLMACY----HENNA-----MKRLALEGCASL-RIV-----NKGSLSPLT	336				
QY	360 LAAEGRKEIRRHILQRFSGLSHLRSKFTFCMYCPAVKSLYDLASVSCSEN-----	412				
Db	337 LAAKLAKKEMDELLEEGDSV-----WAYGDASTAYPLAKPIDINTETIGELNEA	387				


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Db 217 KTTDQGA-YGGEPLFAACFGKKDYDILIOGAP-NIQ--DSGNTILHCY--- 269
OY 317 DNSAENIALVTSMYDGLLOAGARLCPTVOLEDIRNLODLPKLAKKEGKTEIFRILOR 376
Db 270 -----INVSMSYAVARHNAKPAD-----PHVNHAGFTPLLTATKRGRIPEME- 318
OY 377 EESGSHLSKRFTEWCYGPVAVSLYDLASVDSCE-----ENSVLEIARHCSPRHR 429
Db 319 -----IMRVFWRFSMDTCSAFLPLNTLDTIOPDGSSTNDASALMTVI--NGSTPEHLD 368
OY 430 MVVLEPLNKLQAKWDLIPKFLNLCNLIMYFI-FTAVAYHQPCLKQAAPHKAEVG 488
Db 369 MIGSEVIRLADKKAKAOKRIERLVLIYOLITLSIVYIRPT-----ELPRLYMDP 424
OY 489 NSMLTGHILILGLIGYLLVGLQWYFMRHVEIWSFIDSYFEILFEOALLTV----- 542
Db 425 Q-----WDYIRACCELLTILNCFIVGYOOLG 452
OY 543 -----VSQVLCFLAIEWYL-----PLVSAVLVGLNL 570
Db 453 EIRFOGMGYLRNKTAPAKAVFCIANFLLCIPFLMKRHEIEALFVAFALGSMIFL 512
OY 571 LYTRGFQHTGYSVMLOKVLRLDLRLIYLVFLGEFAVA--LYSLSGAMRPEAPTG 628
Db 513 LFPARSAKLTCPVOMIYSIAGDMIRATISAFIVSFQVYFVGKMDAKKLEDTN 572
OY 629 PNATESVQPMGEQDEGNGAOYRGILEASLELFFETIGMELAFQOULHFRGAVLLLLA 688
Db 573 PHACR-----ISGY-----TIYTNPEPEFIFLFRASMGVYEEFSCANVALKTLFVL 624
OY 689 YVLLTYILLMLINLSEYTNVATDSWSIWKLOKA--ISVLEMENGYMKCRKORAGV 746
Db 625 YMFAPIMIMILLAMGMNTYTVIAQEKAMROOYAOIYVLEBSVG-----KERLAAS 679
OY 747 MLTVGTRPD 755
Db 680 QLEYSIRD 688

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RESULT 6
T24772
hypothetical protein T10B10.7 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
C:Accession: T24772
R:Sim, M.
submitted to the EMBL Data Library, May 1996
A:Reference number: Z19934
A:Accession: T24772
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-519 <WIL>
A:Cross-references: EMBL:Z72514; PDB:CAA96679.1; GSPDB:GN00028; CESP:T10B10.7
A:Experimental source: clone T10B10
C:Genetics:
A:Gene: CESP:T10B10.7
A:Map position: X
A:Introns: 47/3; 183/1; 215/2; 249/2; 385/3; 440/3

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Query Match 6.08; Score 261; DB 2; Length 519;
Best Local Similarity 31.28; Pred. No. 4.6e-11;
Matches 90; Conservative 32; Mismatches 96; Indels 70; Gaps 12;
OY 217 TDVYR--GSHALHAIERKSLQCVKLVENGANVHARACGRF---OKGGT----- 264
Db 178 SEETAYAVGSLPHQAIYVNDLEKVTFLCKRGADVHOKRGSEFCADDOKASRTDSIEHE 237
OY 265 -----CFYGEPLSLAACKTQND---VSYLLENPHOPASLOATDSOGNTVL 309
Db 238 WVDLVOSTKTYTGMYGCEYPLSFAACTNGVDCFRLLRAMKADPNMP-----DJNGTIVL 291

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OY 310 HALVMSNSAENIALVTSMYDGLLOAGARLCPTVOLEDIRNLODLPKLAKKEGKTEI 369
Db 292 H-LTVIHD-----LPEMFALVELGANTL-----HVRNNKLTFLLAARAKKHI 335
OY 370 FRHIIQREFSLSHLSKRFTEWCYGPVAVSLYDLASVDSCE-----NSVLEIARHC 422
Db 336 YDLIECDMD-----ISMRYGPVYCAKAPLNDVDITNESDGLNPNSVIANVYGD 386
OY 423 KSPHRHRAVLEPLNKLQAKWDLIPKFLNLCNLIMYFI-FTAVAY 470
Db 387 KVDHLEFFDGL--IEVLESKMEITGKQLEMSLAGIY---FLAVFY 429

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RESULT 7
T19552
hypothetical protein C29E6.2 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C:Accession: T19552
R:Dobson, R.
submitted to the EMBL Data Library, May 1996
A:Reference number: Z19141
A:Accession: T19552
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1188 <WIL>
A:Cross-references: EMBL:Z72504; PDB:CAA96603.1; GSPDB:GN00022; CESP:C29E6.2
A:Experimental source: clone C29E6
C:Genetics:
A:Gene: CESP:C29E6.2
A:Map position: 4
A:Introns: 147/2; 473/3; 500/1; 529/1; 584/2; 688/2; 839/3; 975/3; 1132/3

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Query Match 4.68; Score 200.5; DB 2; Length 1188;
Best Local Similarity 19.38; Pred. No. 2.6e-06;
Matches 135; Conservative 97; Mismatches 207; Indels 261; Gaps 36;

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OY 223 GSHALHAIERKSLQCVKLVENGANVHARACGRF---OKGGT----- 261
Db 518 GNSALHLAARSGHATKVLINDGADKEAKSYOKTPLQVAVDSGKLETQRLVAKGQOI 577
OY 262 -----QGTCTYGEPLSLAACKTQND---VSYLLENPHOPASLOATDSOGNTVL 311
Db 578 ESSSDTKVTLHTAFYGN-----SIYRYFIA--EGVTRDRDECKT---A 619
OY 312 LVMSDNSAENIA--LVTSMYDGLLOAGARLCPTVOLEDIR---NLODLPKLAKKEG 365
Db 620 FDIACENDHVDVARAFLETQWKMLTP---CDVIPDKHRNPVNMKRRTP----- 667
OY 366 KIEIFRHILOREFSLSHLSKRFTEWCYGPVAVSLYDLAS--VDSCE-----EENSYLEI 418
Db 668 -----FRLTL-----TKRPE-----LASVMDNCIEKSEEDSTQSV 700
OY 419 AFH-----CKSPH-----RHRVY 432
Db 701 AYNFEFLDPTVMKRCVSDGCTGEOLICKSAYDEDFKLEKDAQSYASNYDRVYVHPLKL 760
OY 433 L-----EPLNK-LLOAKWDL-IPKFLNLCNLIMYFI-FTAVAYHQPVL----- 475
Db 761 MADAEKHLHLNHPLSKALLKYNRKLGRPMYFALFMYLFIYVSLTOYVRHTRKAPYVWN 820
OY 476 -----KROAPHLKAEVNSMLTGHILIGYLLVGLQWYFMRHVEI--W 522
Db 821 EESYVSEYFDENETGQINTKPD--VVKIITQIALVOCLIEGQOLFQKFAIYVNW 878
OY 523 ISFDISYFELFQ-ALLTVSQCFLF-----LAIEYVLEPLVSAVLGMLNLYYTRGF 577
Db 879 ENMID-----CFIYSTRALIVYDFSECSATSGVQNMOWIILALCIFGGINILFMRKM 933
OY 578 QHNGIYSVMLOKVLRLDLRLIYLVFLGEFAVALVSLQEARPEAPF---GNATES 634
Db 934 PRFGIFVQMFVDIV-KTFEFPFVFLVETIAFSSSFYVILON--RPESTIFMSPLKTV 990

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OY 635 VQPMGEDEGNGAQRKIGLEASLEKFTTGMEGLAFQEOJLHRCM-----VLLLL 686
DB 991 M--WIG-----FEFT---GIFHDEFTTHAEKMPAHTAVACALF 1026
OY 687 LAYLLVYILLNLMLMSETVNSVATDSMISKKLAKAIS-VLEME----- 732
DB 1027 FFFCIITLMLNLVLAVLDIGV--QEKALRLAMQDLVLQIEASLHFFIORTKRY 1085
OY 733 -----NGY--WMCRRKQAGVMTVGTCPD 755
DB 1086 ATCRVATFPYKGLHKTGFAGMWSNFRFRFC--LSVSTDPE 1123

RESULT 8
JH0588
calmodulin-binding protein trpl - fruit fly (Drosophila melanogaster)
C:Species: Drosophila melanogaster
C>Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 24-Sep-1998
C:Accession: JH0588
R:Phillips, A.M.; Bull, A.; Kelly, L.E.
Neuron 8, 631-642, 1992
A>Title: Identification of a Drosophila gene encoding a calmodulin-binding protein with
A:Reference number: JH0588; MID:92232293
A:Accession: JH0588
A>Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-1124 <PHI>
A:Cross-references: GB:M88185; NID:9469057; PID:9158715
A:Experimental source: head
C:Genetics:
A:Gene: trpl
A:Cross-references: FlyBase:FBgn0005614
C:Keywords: calmodulin binding; phosphoprotein; transmembrane protein
F:341-362/Domain: transmembrane #status predicted <TM1>
F:374-396/Domain: transmembrane #status predicted <TM2>
F:462-479/Domain: transmembrane #status predicted <TM3>
F:512-533/Domain: transmembrane #status predicted <TM4>
F:549-572/Domain: transmembrane #status predicted <TM5>
F:643-668/Domain: transmembrane #status predicted <TM6>
F:710-727/809-825/Region: calmodulin binding #status predicted
F:722/Binding site: phosphate (Ser) (covalent) #status predicted

Query Match 4.5%; Score 197.5; DB 2; Length 1124;
Best Local Similarity 19.7%; Pred. No. 4e-06;
Matches 162; Conservative 130; Mismatches 281; Indels 249; Gaps 38;

OY 191 VNACILPLQIDRDSGNPPL-----VNAOCTDD 219
DB 25 VGGCCVPL-----GLPPLLEKKFLLAVERGDMVVRILQKALRHQINICMDP 77
OY 220 YRGHSAHIAIEKRSLOCVKLLVENG-----ANVHARAC-----GRFFQK 261
DB 78 L--GRALTLADNLELVAVGVETKDLALHAINAEVAVELLLEHLLYKES 135
OY 262 Q-----GTCFFGEL--PLSLACTKQMDVSYLLEN-----PH-----OPASL 298
DB 136 EPYSMOKVDINAMFADITPLMLAANKNFELRIILDRGAAPVPHDIRGCECVRL 195
OY 299 QATDSQGNVLH-----ALVWISNLSAENIALVSMYDGLQAAARLCPTVQLED 348
DB 196 TAEDESRHSLSRVNITRALCSPLICLTISNDPSSTAFQJLWELRNALTEOECKSTYKML 255
OY 349 IRNLQ-----DLPLKLAAEKETI-----FRHILQREPSGLSHSRKFTENC 392
DB 256 RROCKKFAVDLDDORTSMELAILIINYDPQMSYERGDMSLRLVQAIKYOKKVV--A 313
OY 393 YCPVAVSL-----YDLASVDSCEENSVLEITAFHCKSPHRRHNVLEPLKKL-----QAK 443
DB 314 HSNITQSSSIWYD--GLPGRKRSIVDKVI--CIA-----QVAVLEPLCYCLAYMCAPCR 365
OY 444 WDLIPKFLNLCN-----LIYMFIFTAVA-----YHOPILKKQAAPHLRAEVGN 489

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DB 366 TGOIMRRKPFMKFLIHASSYLFFILLVLSQRADDPFRIGTRRMKELAEQELRQGO 425
OY 490 SMLTGHILLILGGIYLLVGOIWMFRRHVTWISFIDSYEILFLQALL--TVSQVL 547
DB 426 ---TPSKLELIYMYV---IGFVMEVQEIFAVGMSYLRNMNFIIDLRLNSLYSYM 477
OY 548 CFLAIEW-----YLP-----LLVSALVGMNLLLYTRGQ 578
DB 478 CLRFAIYIQQTETARPQOMAYIPREKHDPDQLIEGLEFAANVSAKLVLHFSINP 537
OY 579 HTGIYSWIOKVIILRDLRFLLIYLVLEFGFVALVLSQEAW-----REAPGTGNAT 632
DB 538 HLGFLQISLGRMY-DIKKFFIYIVLFNA---CGINQLMFLPALEKSKCYLDG-- 591
OY 633 ESVPMEGDEGNGA-----QYRGLIASLELFFETIGMGL-----AFQEOJLHFR 679
DB 592 -----GADWMSGHSDSCMKRRFGNLFESSQSLFVNASFGVGLDDPELSGKSYTRFW 644
OY 680 GMVLLLLAYVLYILLNLMLMSETVNSVATDSMISKKLAKAISYLEMNGYWCRR 739
DB 645 G--LLMGSTSVINIVILLNLMLMSNSTAMIDEHSDTEWKFAR-----TKLMMSY 694
OY 740 KKQAGVMTVGTCPDGPSPERMCFRV-----EEVNMASMEQTLPTLC 782
DB 695 FEDSA-----TLPPFNVLPSYKVIIRIFRKSSTIDRQSKRKEQDFSEYDINMSLV 750
OY 783 EDBSGAVPRTLENPVLASPKEDD--DGASENVYVQQLQ 822
DB 751 W-RYVAAHRRFEN---NPVSEDDINEVKSSEINTMYEMLE 787

RESULT 9
JN0015
trp protein - fruit fly (Drosophila melanogaster)
C:Species: Drosophila melanogaster
C>Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 02-Feb-2001
C:Accession: JN0015
R:Mong, F.; Schaefer, E.L.; Koop, B.C.; Lahendola, J.N.; Johnson-Seaton, D.; Shao, D.
Neuron 3, 81-94, 1989
A>Title: Proper function of the Drosophila trp gene product during pupal development
A:Reference number: JN0015; MID:90148782
A:Accession: JN0015
A:Molecule type: mRNA
A:Residues: 1-1274 <RON>
C:Comment: This photoreceptor membrane-associated protein is not required for the ommatidia
C:Genetics:
A:Gene: trp
A:Cross-references: FlyBase:FBgn0003861
A:Map position: 99C5-6
C:Superfamily: TRPC protein
C:Keywords: glycoprotein; nucleotide binding; P-loop; phosphoprotein; transmembrane P
F:1257-1263/Region: nucleotide-binding motif A (P-loop)
F:64/70/899/Binding site: carboxylate (Asn) (covalent) #status predicted
F:191/602/880/883/924/Binding site: phosphate (Ser) (covalent) #status predicted
F:800/1266/Binding site: phosphate (Thr) (covalent) #status predicted

Query Match 4.4%; Score 191; DB 2; Length 1274;
Best Local Similarity 20.2%; Pred. No. 1.3e-05;
Matches 134; Conservative 99; Mismatches 237; Indels 192; Gaps 30;

OY 213 NAOCTDYYRGSAHIAIEKRSLOCVKLLVENGAVYHARACRFQKQGCFCYFGEIP 272
DB 62 NINCIDPMNR--SALISALENEFDLMLVLEHNIEV-----GDALLHAISEY 108
OY 273 LSLACTKQMDVSYLLENPHQASLOATDSQGN-----VLHAIWISNLSAENIALVTS 328
DB 109 VAVEELLQMEETNH--KEGOPYSEAVDRSKSTPTVDTIFLLLAHANNNEILKI--- 162
OY 329 MYDGLQAAARL-----CPTVQLED-----IRNLQDLPLKLAKEG 365
DB 163 ---LLDRGATLPMHVDYKGCDECVTSQTDSLRLHSQSRINAYRALSSALSSALSSRDP 218

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QY	366	KIEIFRHLIOREFGSLHSKREPMWCGVARSILYDAS--VDSCEBNSVLEIIFRHC	423
Db	219	VLTAFQ--LSMELKRLQAMSEFPAAE-YTERKQVOWFGSILDHATSMLEVMLENFH	275
QY	424	SP-----HRRHVVLEP-LNKLLQAKWDLTPK-----	451
Db	276	EPSHDIWCLASSETLERLKAIRKQKOTFVAHPVVOOLLAAIYWDGLPGFPOEASOOLMD	335
QY	452	FLNELCNL-IYMFIFTAVAHOPFLKQAPHLK-AEVSNSMLTG-----HIIILL	501
Db	336	VYKGGCEFPIT-----SKTIILAPDSEGAKEFMPNPASSSSRTCCSTNPFMLL	383
QY	502	GGIYLLVGOL-----WTF-----WRRH-----VF-----	520
Db	384	GAASLRYVOITFEELAPPMMLTMDLRKHERGSLPGEIILAITTYMALIFEELKLSYS	443
QY	521	-----IW--ISFISYFELLELE--QALLTVYSOVCFPLATEYL-----PL	558
Db	444	DGLFEYIMDLNIVDYISNNEYTWMLICRATAMVYIHRDMLENGIDYEPREHHMPDPD	503
QY	559	LVS-----ALVIGMLNLVYTRQFOHTGITYSMIOKVIIRLDLRELLIYVLEFGHAVA	612
Db	504	LISGAPAGAVNFSYKLVHIFSINPHGLQYSLGMMI-DIIKFFPIYTLVLFNFG--	560
QY	613	LVLSIQAMRPEAPTGNGNALESVQPMEGDDEGNGA-----QYRGILEASLELFKTTIG	667
Db	561	-CGINOLMW-YAELEKNKCYHLHPDVADDDDEKACTIWRRSNLFETSQSLEFMSFGL	618
QY	668	GELLAFOE---QLHFRGMVLLLLIYVLLIYIILLNMLLIMSETVNSVDSMSIMKQ	723
Db	619	VDLVSFPLAGIKSTRRWALLMGFSYSVINIYVLLNMLIMMENSQOIIISERADTEMKFA	678
QY	724	KA 725	
Db	679	RS 680	

RESULT 10

trp protein - fruit fly (*Drosophila melanogaster*)

C:Species: *Drosophila melanogaster*

C:Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 17-Nov-2000

C:Accession: J000092

R:Montell, C.; Rubin, G.M.

Neuron 2, 1313-1323, 1989

A:Title: Molecular characterisation of the *Drosophila* trp locus: a putative integral membrane protein

A:Reference number: J000092; MID:90180449

A:Accession: J000092

A:Molecule type: mRNA

A:Residues: 1-1275 <MON>

A:Experimental source: strain Oregon R

C:Comment: trp protein is expressed predominantly in the rhabdomeric membranes of the photoreceptor

C:Genetics:

A:Gene: trp

A:Cross-references: FlyBase:FBgn0003861

C:Superfamily: TRPC3 protein

C:Keywords: transmembrane protein

F:334-354/Domain: transmembrane protein

F:378-401/Domain: transmembrane #status predicted <TM1>

F:419-436/Domain: transmembrane #status predicted <TM2>

F:457-471/Domain: transmembrane #status predicted <TM3>

F:504-527/Domain: transmembrane #status predicted <TM4>

F:612-630/Domain: transmembrane #status predicted <TM5>

F:636-661/Domain: transmembrane #status predicted <TM6>

F:636-661/Domain: transmembrane #status predicted <TM7>

Query Match	4.4%	Score 190.5;	DB 2;	Length 1275;
Best Local Similarity	19.9%;	Pred. No. 1.5e-05;		
Matches 130;	Conservative 98;	Mismatches 253;	Indels 171;	Gaps 27;

QY 213 MNCITDDYRGSHALHIAIEKRSLCCVLLVENCANYHARACGRFQKGGCTCFYEGLP 272

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Db 62 NINCDEPNRR--SALISAIENENDPMVILLENHIEV-----GGALLHAISEBY 108
QY 273 LSLACTQOMVYVSYLLENPHOPASLOATDSOGTV--LHALVMISDENAENIALVTSM 329
Db 109 VEAVEELLQOMETNH--KEGOPYSMWAVDSKSTFVYDTPILLAHRNNVELIKY-- 162
QY 330 YDGLLOAGARL-----CPTVQLEO-----JANILODLPRIKAAKEGK 366
Db 163 ---LLDRATILPMHDVAKCGCDECVTSQTTDSLHNSORINATAYALASASSITALISSDOV 219
QY 367 IEIFRHILQREFSGISLHRSKRETCWCYGPVRSYLDAS--VDSCEENVLEITAFHCKS 424
Db 220 LTAFO--LSWELKRLQAMESEFRAE--YTEMKQWODGFTSLDHAFTSMELVLEVNHE 276
QY 425 P-----HRRHNVLEP--LNLLOAKWDLIRKF----- 451
Db 277 PSHDIWLGQOTLERLKLAIYRKQKFFVAHPVNOQLLAIWDLGFRFRKQASOQLMD 336
QY 452 FLNPLCNLIYFIPTAAVYHOPTLKQOAPHLKAEVGNSMLTGHILILGJYILVAGOL 511
Db 337 VVKIGCSPPRIYSKLXIIILAPDEGAKFMRKPPVKRTIHCSCSM--FLMLLGAASLRVQI 394
QY 512 -----WTF---WRRH-----VF-----I 521
Db 395 TFEELAPFWMLTMLMEDWRKHERGSLPRIELAITTYIMALFEBELKSLYSDGLPEYIMDL 454
QY 522 W--LSFIDSYFELFLP--QALLTVSQQVLCFLAIENYL-----PLVVS-----A 562
Db 455 WNIYDYISNMEYVWMLLCRATAMVYVRHDLMEFRIDIDYFPEHWHMPRLMLSEGAFAG 514
QY 563 LVLMGLMLNLYVTRGFOHTGTGISVWIKQVILIRDLRLFLITLVLPFGFAVALVLSIOEAMR 622
Db 515 WVSFYKLKVHFFSLNPHILGPOVSLGMMI--DIKFEFITYILVFAAG---CGLNOLIMY 570
QY 623 PEATTPRATISVOPMGEQDEGNGA-----QYRGILASLELYKFTTIGGELAFDE-- 674
Db 571 -YAELEKKNKCIYHLPDVAADFDOEKACTIMWRFSNELFETSQSJFMAFSGLVDVLSFDLAG 629
QY 675 -QLHFRRGVWILLAYVLYTILNLNLMISTVNSVATDSIMKLOKA 725
Db 630 IKSTFRMALLMGSIYINITYILNLLNLMASNSVIOIISERADTEKFRARS 681

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RESULT 11
I38361
TRPC1 protein - human
C:Species: Homo sapiens (man)
C:Date: 31-May-1996 #sequence_revision 31-May-1996 #ext_change 04-Sep-1998
C:Accession: I38361
R:Mes, P.D.; Chevessich, J.; Jeromn, A.; Rosenberg, C.; Stetten, G.; Montell, C.
Proc. Natl. Acad. Sci. U.S.A. 92, 9652-9656, 1995
A:Title: TRPC1, a human homolog of a Drosophila store-operated channel.
A:Reference number: I38361; MUID:96003837
A:Accession: I38361
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-810 <RES>
A:Cross-references: EMBL:X89066; NID:g1019786; PID:g1019787
C:Superfamily: TRPC3 protein

Query Match	3.99	Score 169.5	DB 2	Length 810
Best Local Similarity	19.08	Pred. No. 0.00028		
Matches 147	Conservative 122	Mismatches 275	Indels 231	Gaps
QY	86	GVPAGAGTATGGCTGGACTCCAGAGTACTGAGCAAGACA-GCAAGTATCTCACCGA	1444	
DB	4	GIPPRAREAAVG-----TTHPFSSPGAMLTSSGSGSPVGAPPSPGLPPSMAAAMAA	55	
QY	145	CTCGEDLAGLPLEYLTKSTKYLTDSEYREGSGTKCLKAAV-----LNLKQGVNCC--	194	
DB	56	LYPTDLSG-----ASSSLSPSSPSSSSNNEMALKDVREYKEENTLLEKFTLLACDK	1080	

QY 195 -----ILPLQIDRDSGNPQPVNAOCTDDIYRGSHLHAIEKRSLOQCVKLVENGANV 249
 DB 109 GDYVWAKKILE-ENSSGD-----LNINCVD--VLGRNAVTTITENENIDITQILLIDYG--- 158
 QY 250 HARACGRFPQGGCTGF--YFGEPLSLACTQOMDVVSTLE-----NPH----- 293
 DB 159 ----COKLMERIONPEKSTTMDVAPVILAAHRRNNETILMLKODVSLPRPHAVGCECTL 214
 QY 294 -----QPASLOATDSOGNTVLAHVMISD----- 317
 DB 215 CSAKNNKDSLRSFRFDIYRCLASPALIMLTTEE--DPILRAFELSDMLKELVEYEF 272
 QY 318 NSAKENALVTSWMDGLLOAGARLCPTVOLEDIN-----LQDITPKLA 361
 DB 273 NDVEELAROCKMFAKDLLOAR--NSRELEVILNHTSSDPELDRGLLEBRMINSRLKLA 330
 QY 362 AEGKIEIFRHLQREFSGLSLSRKFTWCYGPVRVSLYDLASVDSCEENSVLEITAFH 421
 DB 331 IKYN-----QKEF-----VSQSNCOO--FLNTVWEG 354
 QY 422 CKSPHRHR-----MVYLE-----PLNKL-----QAKWDLIPKFFLNLCLIMYEFIF 465
 DB 355 QMSGYRRKPTCKKIMTVLVGVGFVPLSLCYLAPKRSQFORLIHTPEPMKTIHGASVTFE 414
 QY 466 T-----AAVYHQPTLKAAPHLKAEVGNMMLTGHILLILGCTILLYGOLMYFMRHV 519
 DB 415 LILLNLVSLVYNEDK-----KNTMGPALEIRIDYLL-----WIIGMIMSDIKR-- 458
 QY 520 FTMISFIDSYPE-----ILFLFOA--LITVISOVLCLFLA-----EM--YLPILVSAL 563
 DB 459 -LMYEBLEFLEESRNOQSFVANSYLAFALKVVAHNNKPHDPAKDKDWAEPPTVAES 517
 QY 564 VLGMNLVLYTGTGFOHTGTIYSV-----TQVYLRLDLFLFLIYLFVLFGLFAVALYSLSQ 618
 DB 518 LFAFANVLSYLRLFEWYTTSSILGPLQISMGMLODFGKFLGELLVLESTIGLQVLD 577
 QY 619 EAMREAPRPGNATESVQOMGOEDGNGAQYRGILEASLELFKFTIGGELAF----- 672
 DB 578 KQY-----TSKQKOCQVGFCEQOSNDT--FHSFGTCFALFWYIFSLAHVAIFVTRFS 629
 QY 673 --QEOILHFRGNVLLLLAVLTYLLMLLALMSETVNSVATDSMSIMLKOKA 725
 DB 630 YGEELQSFVGN--IVGYTNVVVVIVLTKLIVAMLMKSFQOLIANNHEDKWKFKARA 682

RESULT 12

T23729
 hypothetical protein M05B5.6 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
 C:Accession: T23729
 R:Gardner, A.
 submitted to the EMBL Data Library, April 1996
 A:Reference number: T23729
 A:Accession: T23729
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-481 <M1>
 A:Cross-references: EMBL:Z71265; PIDN:CAA95836.1; GSPDB:GN00019; CESP:M05B5.6
 A:Experimental source: clone M05B5
 C:Genetics:
 A:Gene: CESP:M05B5.6
 A:Map position: 1
 A:Introns: 50/2; 99/1; 133/3; 185/3; 229/3; 402/3; 457/3

Query Match 3.68; Score 157.5; DB 2; Length 481;

Best Local Similarity 23.08; Pred. No. 0.0011;
Matches 90; Conservative 58; Mismatches 149; Indels 95; Gaps 17;

QY 351 NLQDITPLKLAKEGRIFFRIHLQREFSGLSLSRKFTWCYGPVRVSLYDLASVDSCE 410
 DB 57 NMKELRLKSGKNG--VIRH-----PYILNTVYNOKLIDCAFFYS-- 94

QY 411 ENSVLEIIAIFCKSPHRHRMVLEPLNKLLOAKMDLLIPKFFLNLCLIMYFTTAV 470
 DB 95 -----LHILAF-----LVFLLAHVHSRNLFPDL-----ITLFTGIF 130
 QY 471 HQPTLKQAAAPHKAEVGNMMLTGHILLILGCTILLYGOLMYFMRHVIFWISFIDS 530
 DB 131 MFLVKCT-----IKARITKS-VSTWFIACFENIFTYMATLAVLWLTVE---GYDYHL 182
 QY 531 EILFPLALTVSQCFLAIEWYIFPLVLSALVGLNLLITRGFOHGTISVMTOKV 590
 DB 183 EVKTI-----VWFLEPII--AISAANLLIYMRK--SPGIYIFMTR- 222
 QY 591 ILRLDLFLIYVLFEGFAVALVLSQEAHREAPRGPNATES--VOMEGODEGNG 647
 DB 223 ILRSEHAIATWPTLILAFSPALLIMRDGVKRPWPLIDQOTERMVQTM----- 273
 QY 648 AQYRGILEASLELFKFTIGGELAFQOLHFRGV--LILLAVLTYLLMLLALMS 706
 DB 274 ---LVILQAVTK--TSTMIGEVANDILDTNOMIPSLVLEIIVILMLMVSILAV 328
 QY 707 ETV---NSVATDSMTIKLOKATSVLEMNGY 735
 DB 329 GDVYTNNTPTAODKLKIKVNFVIALQISEQF 360

RESULT 13

T13940
 ankyrin - fruit fly (Drosophila melanogaster)
 C:Species: Drosophila melanogaster
 C>Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 17-Nov-2000
 C:Accession: T13940
 R:Dubreuil, R.R.; Yu, J.
 Proc. Natl. Acad. Sci. U.S.A. 91, 10285-10289, 1994
 A:Title: Ankyrin and beta-spectrin accumulate independently of alpha-spectrin in Dros
 A:Reference number: Z17820; M01D:95024098
 A:Accession: T13940
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-1549 <DDH>
 A:Cross-references: EMBL:L35601; NID:9557083; PID:9557084; PIDN:AAC37208.1
 C:Genetics:
 A:Cross-references: FlyBase:FBgn0011747

Query Match 3.68; Score 157; DB 2; Length 1549;

Best Local Similarity 22.88; Pred. No. 0.0046;
Matches 91; Conservative 61; Mismatches 134; Indels 114; Gaps 17;

QY 161 TSKYLTDSSEYTEGSGTCTIMKRAVLNLDKGVNACIPLQIDRDSGNPQPVNAOCTD 220
 DB 363 TVDYLT-ALHVAAHGCHVAVAKLLLDYKAPNARAL----- 397
 QY 221 YNGSHALHIAIKRSIQCVKLVENGANVHARACGR-----FQKGGCTGYF----- 268
 DB 398 -NGFTPLHACKKNRIKIVWELLIKGANIGATTESGLPLHVASFGCINIYIYLQHA 456
 QY 269 -----GELPLSLAACKQKQDVVSYLENHQHPASLOATDSOGNTVLAHVMISD 320
 DB 457 SADLPTIRGETPLHLAARNQADIRILRS---AKDAIYREQOTPLHVASRIG--- 508
 QY 321 ENIALVTSWMDGLLOAGARLCPTVOLEDIRNQLDPLPLAKKEGRIEFRIILO----- 375
 DB 509 -NINIML-----LLOHGAEI-----NAQSDKYSALHIAKEGQENTVOVLENGAEN 556
 QY 376 -----REFSGLSLSRKFTWCYGPVRVSLYDLASVDSCEENSVLEI-IAFCKSPHRHR 429
 DB 557 NNAVTKGTFPL-HLACKYKQ--QNVVQILLQNGASIDQKNDVPRPLVAHTYNNPSTIVE 613
 QY 430 MVYLEPLNKLLOAKMDLLIPKFFLNLCLIMYFTTAVAHQPTL---KKQAP-HLK 484
 DB 614 ILLKNGSSPNLCAR---NGOCAIHIAKKNYLEIAMOLOHGADVNIISKGSFPLHLA 669

QY 485 AEVGN-----SML-----TGHLL 499
 DB 670 ACGGNDVQVLLLEGVISAANNGLPLHVAAGEGHVLV 709

RESULT 14

H71274

probable ankryrin - syphilis spirochete

C:Species: Treponema pallidum subsp. pallidum (syphilis spirochete)

C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999

C:Accession: H71274

R:Fraser, C.M.; Norris, S.J.; Weinstein, G.M.; White, O.; Sutton, G.G.; Dodson, R.; Gwin
 rson, J.; Khaila, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Utterback, T.; MDDC
 they, L.; Weidman, J.; Smith, H.O.; Venter, J.C.
 Science 281, 375-388, 1998

A:Title: Complete genome sequence of Treponema pallidum, the syphilis spirochete.
 A:Reference number: A71250; MUID:98332770

A:Accession: H71274

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-934 <COL>

A:Cross-references: GB:AE001254; GB:AE000520; NID:g3323148; PIDN:AA05803.1; PID:g332314

A:Experimental source: strain Nichols

C:Genetics:

A:Gene: TP0835

C:Superfamily: syphilis spirochete probable ankryrin; ankryrin repeat homology

F:281-313/Domain: ankryrin repeat homology <AN22>

Query Match 3.5%; Score 154; DB 1; Length 934;
 Best Local Similarity 28.1%; Pred. No. 0.0042;

Matches 62; Conservative 31; Mismatches 78; Indels 50; Gaps 8;

QY 176 GKTCLKKAVLN-----LKDGVNAC-----IPLQIDRDSGNPOPL-----VNA 214
 DB 481 GNTLHYAANDRAVGEFLMREGADIFSTNVHGVSPKLTALTSGRREDMILTANVHA 540
 QY 215 OCTDDYRHSALHIAIEKRSLOQVCLVNGANVHARACGRFQKQGTCEYFGEPLPS 274
 DB 541 ODG-----GNTPLHACEWKLTOANGILRKGAIEARNLNQ-----ETPLF 583
 QY 275 LAQCTKQWVSVYLE-NPHQASLQATDSQGTVHALVMSDNSAENIALVTSNYDGL 333
 DB 584 SAKSDAAEVISTLHPQAGNPALVDARDAVGFVLAHACVHWSAALRSADVL-----I 635
 QY 334 LOAGARLCEPTVOLEDIRNODLPLKLAKEGKIEIFRHIL 374
 DB 636 READAR---HVSLLNARNLSGKPLHLAARAGNVDFIRLL 673

RESULT 15

T42714

ankryrin 3, splice form 2 - mouse

C:Species: Mus musculus (house mouse)

C:Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 04-Mar-2000

C:Accession: T42714

R:Peterson, L.L.; John, K.M.; Lu, F.M.; Elcher, E.M.; Higgins, A.; Yialamas, M.; Turtzo, I

J. Cell Biol. 130, 313-330, 1995

A:Title: Ank3 (epithelial ankryrin), a widely distributed new member of the ankryrin gene

the repeat domain.

A:Reference number: 222237; MUID:95340633

A:Accession: T42714

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-1765 <PEP>

A:Cross-references: EMBL:L40632; NID:g710548; PID:g710551; PIDN:AA01605.1

A:Experimental source: strain C57BL/6J; kidney

C:Genetics:

A:Gene: Ank3

A:Map position: 10

A:Introns: 1587/1

C:Superfamily: ankryrin; ankryrin repeat homology

C:Keywords: alternative splicing

Query Match 3.5%; Score 151; DB 2; Length 1765;
 Best Local Similarity 27.7%; Pred. No. 0.014;
 Matches 78; Conservative 43; Mismatches 91; Indels 70; Gaps 14;

QY 222 RGHSAHLIAIEKRSLOQVCLVNGANVHARACGRFQKQGTCEYFGEPLPSIACTQ 281
 DB 448 RGETALHMAARSGQAEVRYLVQDGAQVEKA-----KDDGT-----PLHISRLK 494
 QY 282 KDVVSYLLENPHRPAQLQATDSQGTVHALVMSDNSAENIALVTSMDGLQAGARLC 341
 DB 495 ADIVQQLQ--QGASPNMATTSGYPLH--LAAREGHEDVAAF-----LUDHGASLS 542
 QY 342 PFVQLEDIRNLODPLPLKLAKEGKIEIFRHILQREES-----GLSHLSRFTFMCYGPVR 397
 DB 543 ITTK-----KGFTPLHVAAKYKGLVVASLQKASAPDAACKSGLT-----PLH 586
 QY 398 VSLYDLASVDSCEENSEYLEIIAFHCKSPRRHRVYLEPINKLQAKWDLIPKFLNPLC 457
 DB 587 VAAH-----YDNQKVALLLDQGASPHAAKNGYPLH--IAAK-----KNQMDIAT 631
 QY 458 NLI-YMFTTAAVAHQPTLKQAAPHLKAEVGN---SMLLT 494
 DB 632 SLEYGADANAV-----TROGIASVHLAAQEGHVDVMSLLS 668

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